GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 02:00:57 ; Search time 2169.11 Seconds
(without alignments)
11147.382 Million cell updates/sec

Title: US-09-623-035-5
Perfect score: 1493
Sequence: 1 tttaaacgggccctctagac.....atgtgttaggaatgtcaaca 1493

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : EST:*
1: em_estba:*
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8: em_htc:*
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10: gb_est2:*
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14: gb_est5:*
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17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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22: em_gss_fun:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
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| | 6 | 746 | 50.0 | 1073 | 14 | BQ051183 | BQ051183 AGENCOURT |
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| | 8 | 737 | 49.4 | 1079 | 13 | BM544653 | BM544653 AGENCOURT |
| | 9 | 724 | 48.5 | 916 | 14 | BQ221490 | BQ221490 AGENCOURT |
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| | 43 | 567 | 38.0 | 593 | 14 | BM822793 | BM822793 K-EST0093 |
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| | 46 | 559 | 37.4 | 727 | 12 | BG499714 | BG499714 602545122 |
| | 47 | 553 | 37.0 | 904 | 12 | BG256208 | BG256208 602369162 |
| | 48 | 550 | 36.8 | 558 | 14 | BM854824 | BM854824 K-EST0137 |
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| | 50 | 535 | 35.8 | 637 | 14 | BM769641 | BM769641 K-EST0052 |
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| | 58 | 505 | 33.8 | 866 | 12 | BG622131 | BG622131 602646752 |
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| | 67 | 485 | 32.5 | 595 | 10 | AV703419 | AV703419 AV703419 |
| | 68 | 484 | 32.4 | 551 | 12 | BG536051 | BG536051 602564327 |
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| | 72 | 473 | 31.7 | 524 | 10 | AW850720 | AW850720 IL3-CT021 |
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| | 74 | 471 | 31.5 | 1054 | 14 | BM925410 | BM925410 AGENCOURT |
| | 75 | 470 | 31.5 | 621 | 10 | AW361987 | AW361987 PM2-CT026 |
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| | 104 | 385 | 25.8 | 536 | 9 | AA188213 AA188213 zp80e09.r |
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| c | 112 | 372 | 24.9 | 634 | 10 | AW578438 AW578438 RC1-CT024 |
| c | 113 | 372 | 24.9 | 634 | 10 | AW604387 AW604387 RC1-CT024 |
| | 114 | 370 | 24.8 | 510 | 9 | AU140068 AU140068 AU140068 |
| c | 115 | 363 | 24.3 | 411 | 9 | AI765154 AI765154 wi48h07.x |
| | 116 | 363 | 24.3 | 479 | 14 | R80350 R80350 yi96e01.r1 |
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| | 129 | 344 | 23.0 | 441 | 14 | H73378 H73378 yu48f12.s1 |
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| | 136 | 333 | 22.3 | 370 | 9 | AA086066 AA086066 zn64a11.r |
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| | 164 | 278 | 18.6 | 329 | 10 | BE243890 BE243890 TCBAP1E15 |
| | 165 | 275 | 18.4 | 359 | 10 | BE245283 BE245283 TCBAP1E24 |
| | 166 | 275 | 18.4 | 708 | 13 | BI094403 BI094403 602856233 |
| | 167 | 271 | 18.2 | 729 | 12 | BG548095 BG548095 602575829 |
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| | 169 | 270 | 18.1 | 371 | 13 | BI057763 BI057763 PM0-GN034 |
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| | 257 | 156 | 10.4 | 372 | 12 | BG899212 |
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ALIGNMENTS

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DEFINITION  AL550277 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI039YF15 5
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ACCESSION   AL550277
VERSION     AL550277.1  GI:12887094
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1074)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1074
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                     /db_xref="taxon:9606"
                     /clone="CS0DI039YF15"
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                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      312 a    257 c    238 g    264 t      3 others
ORIGIN

  Query Match             63.6%;  Score 950;  DB 9;  Length 1074;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1000;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 60

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
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Db     61 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTVGCCTTCCCCC 120

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
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Db    121 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 180

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
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Db    181 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 240

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
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Db    241 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 300

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
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Db    301 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 360

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
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Db    361 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 420

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
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Db    421 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 480

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
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Db    541 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 600

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Db    601 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 660

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Db    661 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 720

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
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Db     841 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 900

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
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Db     901 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 960

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTT 1198
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RESULT 2
AL575907/c
LOCUS       AL575907               1000 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL575907 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI067YL02 3
            prime, mRNA sequence.
ACCESSION   AL575907
VERSION     AL575907.1  GI:12937532
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1).301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      249 a    205 c    225 g    319 t      2 others
ORIGIN

  Query Match           58.0%;  Score 866;  DB 9;  Length 1000;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  966;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy     488 GCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGA 547
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Db     909 GCTGCGAGGTGCCAACAAGGCTTAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGA 850

Qy     548 ATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAAC 607
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Db     849 ATTATCTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAAC 790

Qy     608 CTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAAT 667
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Db     789 CTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAAT 730

Qy     668 TTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTAC 727
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Db     729 TTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTAC 670

Qy     728 CAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTAT 787
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Db     669 CAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTAT 610

Qy     788 TTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGT 847
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Db     609 TTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGT 550

Qy     848 TGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTC 907
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Db     549 TGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTC 490

Qy     908 AAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGAT 967
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Db     489 AAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGAT 430

Qy     968 TCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGA 1027
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Db     429 TCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGA 370

Qy    1028 GTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTC 1087
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Db     369 GTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTC 310

Qy    1088 AGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCA 1147
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Db     309 AGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCA 250

Qy    1148 CCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAA 1207
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Db     249 CCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAA 190

Qy    1208 CCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCC 1267
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Db     189 CCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCC 130

Qy    1268 GTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCA 1327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 GTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCA 70

Qy    1328 TGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACT 1387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 TGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACT 10

Qy    1388 GTTCCTAG 1395
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Db       9 GTTCCTAG 2


RESULT 3
AL542661
LOCUS       AL542661               1003 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL542661 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE014YB04 5 prime
            , mRNA sequence.
ACCESSION   AL542661
VERSION     AL542661.1  GI:12874926
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
```

```
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .1003
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                     /clone="CS0DE014YB04"
                     /clone_lib="LTI_FL002_PL1"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      278 a    239 c    233 g    247 t      6 others
ORIGIN

  Query Match            56.4%;  Score 842;  DB 9;  Length 1003;
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Db      1 GCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCT 60

Qy    252 GCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCT 311
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Db     61 GCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCT 120

Qy    312 TCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGA 371
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGA 180

Qy    372 TACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTC 431
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Db    181 TACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTC 240

Qy    432 AGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTG 491
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Qy    552 TTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTC 611
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Db    361 TTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTC 420

Qy    612 TCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTG 671
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Db    421 TCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTG 480

Qy    672 TAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGG 731
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Db    481 TAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGG 540

Qy    732 TGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGG 791
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Db    541 TGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGG 600

Qy    792 CTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCC 851
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Qy    972 CATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGG 1031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGG 840

Qy   1032 CC 1033
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Db    841 CC 842


RESULT 4
AL543593
LOCUS       AL543593                927 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL543593 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI006YE18 5
            prime, mRNA sequence.
ACCESSION   AL543593
VERSION     AL543593.1  GI:12876072
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                     /db_xref="taxon:9606"
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                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      248 a    217 c    224 g    237 t      1 others
ORIGIN

  Query Match            52.4%;  Score 782;  DB 9;  Length 927;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  902;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    173 GCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGC 232
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Db     61 TGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCG 120

Qy    293 TGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCC 352
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Db    121 TGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCC 180

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAG 300

Qy        473 AGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGC 532
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Db        301 AGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGC 360

Qy        533 CTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAG 592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAG 420

Qy        593 GTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGT 652
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGT 480

Qy        653 CCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATG 712
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATG 540

Qy        713 GTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACA 772
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        541 GTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAA-CATCTCCTTCTCATGTAACA 599

Qy        773 CAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCC 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 CAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCC 659

Qy        833 AGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTG 892
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 AGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTG 719

Qy        893 ACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATG 952
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 ACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATG 779

Qy        953 CATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATG 1012
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        780 CATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATG 839

Qy       1013 ATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGG 1072
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        840 ATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGG 899

Qy       1073 TCC 1075
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Db        900 TCC 902

RESULT 5
BM806293
LOCUS       BM806293                1025 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6542718 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548732
            5', mRNA sequence.
ACCESSION   BM806293
VERSION     BM806293.1  GI:19123116
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1025)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12258  row: c  column: 05
            High quality sequence stop: 713.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5548732"
                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
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                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.  Library constructed by Life
                     Technologies."
BASE COUNT      253 a    260 c    254 g    254 t      4 others
ORIGIN

  Query Match             50.0%;  Score 747;  DB 14;  Length 1025;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  747;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 90

Qy        198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 150

Qy        258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 210

Qy        318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
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Db        211 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 270

Qy        378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 330

Qy        438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
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Db        331 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 390

Qy        498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 450

Qy        558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 510

Qy        618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 570

Qy        678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 630

Qy        738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 690

Qy        798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 750
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Qy     858 CAGAGAAATTTATTGTCCAGCACCACC 884
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Db     751 CAGAGAAATTTATTGTCCAGCACCACC 777


RESULT 6
BQ051183
LOCUS       BQ051183                1073 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6763621 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5792538
            5', mRNA sequence.
ACCESSION   BQ051183
VERSION     BQ051183.1  GI:19810523
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12891  row: a  column: 19
            High quality sequence stop: 628.
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                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      321 a    275 c    227 g    250 t
ORIGIN

  Query Match           50.0%;  Score 746;  DB 14;  Length 1073;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  746;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     418 GGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTC 477
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      12 GGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTC 71

Qy     478 TGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTAT 537
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      72 TGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTAT 131

Qy     538 ATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC 597
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     132 ATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC 191

Qy     598 AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACA 657
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     192 AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACA 251

Qy     658 GCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAG 717
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Db     252 GCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAG 311

Qy     718 ATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGG 777
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Db     312 ATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGG 371

Qy     778 TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGG 837
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     372 TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGG 431

Qy     838 AGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAAT 897
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     432 AGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAAT 491

Qy     898 GGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGT 957
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Db     492 GGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGT 551

Qy     958 AATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAA 1017
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Db     552 AATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAA 611

Qy    1018 GGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCA 1077
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Db     612 GGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCA 671

Qy    1078 CCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCT 1137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     672 CCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCT 731

Qy    1138 CAGAAAACCACCACAAAAACCACCAC 1163
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Db     732 CAGAAAACCACCACAAAAACCACCAC 757


RESULT 7
BQ216954
LOCUS       BQ216954                912 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7549174 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059366
            5', mRNA sequence.
ACCESSION   BQ216954
VERSION     BQ216954.1  GI:20398354
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13325  row: o  column: 15
            High quality sequence stop: 614.
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                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      224 a    218 c    233 g    236 t      1 others
ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy     201 GACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCT 260
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Db      61 GACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCT 120

Qy     261 GCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGA 320
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Db     121 GCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGA 180

Qy     321 TGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAAT 380
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Db     181 TGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAAT 240

Qy     381 AACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTG 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTG 300

Qy     441 CCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCC 500
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Db     301 CCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCC 360

Qy     501 AACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGT 560
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Db     361 AACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGT 420

Qy     561 CGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACC 620
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Db     421 CGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACC 480

Qy     621 AAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAA 680
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Db     481 AAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAA 540

Qy     681 ATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATT 740
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Db     541 ATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATT 600

Qy     741 ATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTC 800
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Db     601 ATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTC 660

Qy     801 TAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAG 860
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Db     661 TAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAG 720

Qy     861 AGAAATTTATTGTCCAGCACCACC 884
           ||||||||||||||||||||||||
Db     721 AGAAATTTATTGTCCAGCACCACC 744


RESULT 8
BM544653
LOCUS       BM544653                1079 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6494695 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727356
            5', mRNA sequence.
ACCESSION   BM544653
VERSION     BM544653.1  GI:18776079
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1079)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12721  row: e  column: 21
            High quality sequence stop: 724.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5727356"
                     /clone_lib="NIH_MGC_124"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
                     (destroyed); Site_2: NotI; RNA source male hippocampus,
                     age 27. Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.4 kb, insert size range 0.9-4 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 012."
BASE COUNT      286 a    274 c    252 g    265 t      2 others
ORIGIN

  Query Match             49.4%;  Score 737;  DB 13;  Length 1079;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  737;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     158 CGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGA 217
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Db      47 CGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGA 106

Qy     218 GCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGT 277
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Db     107 GCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGT 166

Qy     278 TGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGC 337
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Db     167 TGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGC 226

Qy     338 CAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAG 397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     227 CAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAG 286

Qy     398 AAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAAT 457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     287 AAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAAT 346

Qy     458 GGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTG 517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     347 GGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTG 406

Qy     518 CATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAAT 577
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     407 CATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAAT 466

Qy     578 ATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTC 637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     467 ATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTC 526

Qy     638 AGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGG 697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     527 AGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGG 586

Qy     698 GAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCT 757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     587 GAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCT 646
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Qy     758 CCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTT 817
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     647 CCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTT 706

Qy     818 CAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAG 877
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     707 CAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAG 766

Qy     878 CACCACCACAAATTGAC 894
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Db     767 CACCACCACAAATTGAC 783


RESULT 9
BQ221490
LOCUS       BQ221490                916 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7567431 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060184
            5', mRNA sequence.
ACCESSION   BQ221490
VERSION     BQ221490.1  GI:20402890
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13328  row: a  column: 17
            High quality sequence stop: 662.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6060184"
                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      236 a    214 c    232 g    234 t
ORIGIN

  Query Match           48.5%;  Score 724;  DB 14;  Length 916;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  724;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     161 AGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCG 220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCG 60

Qy     221 TGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGT 280
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Db      61 TGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGT 120

Qy     281 GCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAG 340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAG 180

Qy     341 CTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAA 400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAA 240

Qy     401 GCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGT 460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGT 300

Qy     461 CAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCAT 520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCAT 360

Qy     521 CCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATG 580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATG 420

Qy     581 AGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGA 640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGA 480

Qy     641 ATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAG 700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAG 540

Qy     701 AAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCT 760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCT 600

Qy     761 TCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAG 820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAG 660

Qy     821 GCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCAC 880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCAC 720

Qy     881 CACC 884
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Db     721 CACC 724


RESULT 10
BQ228452
LOCUS       BQ228452                880 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7657435 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059688
            5', mRNA sequence.
ACCESSION   BQ228452
VERSION     BQ228452.1  GI:20409852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13326  row: m  column: 01
            High quality sequence stop: 615.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6059688"
                     /clone_lib="NIH_MGC_68"
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                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      286 a    200 c    175 g    219 t
ORIGIN

  Query Match             48.2%;  Score 720;  DB 14;  Length 880;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  720;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     579 TGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCA 638
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCA 60

Qy     639 GAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGG 698
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGG 120

Qy     699 AGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTC 758
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTC 180

Qy     759 CTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTC 818
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTC 240

Qy     819 AGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGC 878
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGC 300

Qy     879 ACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACA 938
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACA 360

Qy     939 GTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTG 998
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTG 420

Qy     999 TACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATC 1058
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATC 480

Qy    1059 TCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTAC 1118
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTAC 540

Qy    1119 AGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGC 1178
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGC 600

Qy    1179 AACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAA 1238
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAA 660

Qy    1239 AGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTT 1298
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTT 720


RESULT 11
BQ051318
LOCUS       BQ051318                1016 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6763612 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5792705
            5', mRNA sequence.
ACCESSION   BQ051318
VERSION     BQ051318.1  GI:19810658
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1016)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12891  row: h  column: 18
            High quality sequence stop: 642.
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5792705"
                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      279 a    252 c    226 g    259 t
ORIGIN

  Query Match             48.1%;  Score 718;  DB 14;  Length 1016;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  718;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     196 GCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCC 255
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCC 60

Qy     256 CGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCC 315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCC 120

Qy     316 CCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACT 375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACT 180

Qy     376 GTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTG 435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTG 240

Qy     436 ATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAG 495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAG 300

Qy     496 GTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTT 555
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Db     301 GTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTT 360

Qy     556 CCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTA 615
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTA 420

Qy     616 TCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAA 675
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Db     421 TCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAA 480

Qy     676 AAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGC 735
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Db     481 AAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGC 540

Qy     736 ATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCG 795
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Db     541 ATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCG 600

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Db     601 ACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAG 660

Qy     856 TGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 913
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Db     661 TGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 718


RESULT 12
AL541261
LOCUS       AL541261                862 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL541261 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005YG14 5 prime
            , mRNA sequence.
ACCESSION   AL541261
VERSION     AL541261.1  GI:12872159
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 862)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .862
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DE005YG14"
                     /clone_lib="LTI_FL002_PL1"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      216 a    204 c    217 g    224 t      1 others
ORIGIN

  Query Match            47.9%;  Score 715;  DB 9;  Length 862;
  Best Local Similarity  99.9%;  Pred. No. 0;
  Matches  835;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy     148 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 207
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Db      13 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 72

Qy     208 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 267
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 132

Qy     268 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 192

Qy     328 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 252

Qy     388 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     253 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 312

Qy     448 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 507
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Db     313 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 372

Qy     508 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 567
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Db     373 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 432

Qy     568 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 627
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     433 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 492

Qy     628 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 687
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Db     493 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 552

Qy     688 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 747
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Db     553 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 612

Qy     748 GCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTT 807
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Db     613 GCAA-CATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTT 671

Qy     808 TGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATT 867
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Db     672 TGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATT 731

Qy     868 TATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTAT 927
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Qy     928 GGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGA 983
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Db     792 GGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGA 847


RESULT 13
AL541069
LOCUS       AL541069                849 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL541069 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005YG07 5 prime
            , mRNA sequence.
ACCESSION   AL541069
VERSION     AL541069.1  GI:12871785
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 849)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .849
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                     /clone="CS0DE005YG07"
                     /clone_lib="LTI_FL002_PL1"
                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
```

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                    , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                    fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com"
BASE COUNT      215 a    201 c    211 g    221 t      1 others
ORIGIN

  Query Match             47.4%;  Score 707;  DB 9;  Length 849;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  827;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    151 GACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCG 210
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Qy    271 GTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAAT 330
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Db    121 GTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAAT 180

Qy    331 GCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAA 390
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Db    181 GCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAA 240

Qy    391 TGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGC 450
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Qy    451 AGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTA 510
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Db    301 AGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTA 360

Qy    511 AATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTT 570
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Db    361 AATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTT 420

Qy    571 GTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACT 630
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Db    421 GTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACT 480

Qy    631 TGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCT 690
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Db    481 TGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCT 540

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Db    541 AATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCA 600

Qy    751 ACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGT 810
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Qy    811 CTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTAT 870
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Db    660 CTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTAT 719

Qy    871 TGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGA 930
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Qy    931 TATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATT 978
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RESULT 14
AL547998
LOCUS       AL547998                884 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL547998 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI035YJ20 5
            prime, mRNA sequence.
ACCESSION   AL547998
VERSION     AL547998.1  GI:12882590
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      247 a    196 c    207 g    231 t      3 others
ORIGIN

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  Best Local Similarity   99.8%;  Pred. No. 0;
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Qy    226 GCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTG 285
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Db      1 GCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTG 60

Qy    286 CCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTG 345
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Qy    406 GTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGAT 465
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Qy    526 AAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGC 585
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Qy    586 CGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTA 645
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Qy    646 AAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATA 705
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Qy    706 CGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCA 765
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Qy     766 TGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGC 825
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Qy     826 TCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCA 885
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Qy     886 CAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTA 945
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DEFINITION  AGENCOURT_6631924 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5757147
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ACCESSION   BM923160
VERSION     BM923160.1  GI:19373539
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12798  row: o  column: 04
            High quality sequence start: 5
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                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      268 a    269 c    248 g    260 t
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Best Local Similarity   100.0%;  Pred. No. 0;
Matches  676;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy     291 CGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGG 350
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Qy     351 CCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAA 410
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Qy     411 AATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGA 470
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GenCore version 5.1.3
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SUMMARIES

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| | 1 | 1356 | 90.8 | 2116 | 1 | US-07-811-048-9 | Sequence 9, Appli |
| | 2 | 1203 | 80.6 | 2847 | 1 | US-08-087-007-2 | Sequence 2, Appli |
| | 3 | 1203 | 80.6 | 2847 | 3 | US-08-483-433-2 | Sequence 2, Appli |
| | 4 | 1203 | 80.6 | 2847 | 5 | PCT-US92-05920-2 | Sequence 2, Appli |
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| | 7 | 1195 | 80.0 | 2096 | 1 | US-08-278-630A-10 | Sequence 10, Appl |
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| | 10 | 970 | 65.0 | 1848 | 4 | US-09-475-460A-31 | Sequence 31, Appl |
| | 11 | 970 | 65.0 | 1848 | 4 | US-09-748-061A-31 | Sequence 31, Appl |
| | 12 | 970 | 65.0 | 1878 | 2 | US-08-435-149-17 | Sequence 17, Appl |
| | 13 | 816 | 54.7 | 969 | 1 | US-08-310-416A-12 | Sequence 12, Appl |
| | 14 | 816 | 54.7 | 969 | 2 | US-08-888-171-12 | Sequence 12, Appl |
| | 15 | 707 | 47.4 | 860 | 1 | US-08-310-416A-19 | Sequence 19, Appl |
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| c | 754 | 17 | 1.1 | 91 | 4 | US-09-168-629-16 | Sequence 16, Appl |
| c | 755 | 17 | 1.1 | 92 | 4 | US-08-974-549A-614 | Sequence 614, App |
| c | 756 | 17 | 1.1 | 144 | 4 | US-09-460-145-7 | Sequence 7, Appli |
| c | 757 | 17 | 1.1 | 228 | 6 | 5273901-10 | Patent No. 5273901 |
| c | 758 | 17 | 1.1 | 228 | 6 | 5482709-9 | Patent No. 5482709 |
| c | 759 | 17 | 1.1 | 264 | 2 | US-08-690-011A-10 | Sequence 10, Appl |
| c | 760 | 17 | 1.1 | 266 | 4 | US-09-299-495F-10 | Sequence 10, Appl |
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| c | 763 | 17 | 1.1 | 294 | 2 | US-08-690-011A-18 | Sequence 18, Appl |
| c | 764 | 17 | 1.1 | 300 | 4 | US-09-299-495F-18 | Sequence 18, Appl |
| c | 765 | 17 | 1.1 | 324 | 4 | US-09-299-495F-14 | Sequence 14, Appl |
| c | 766 | 17 | 1.1 | 327 | 1 | US-08-638-610-3 | Sequence 3, Appli |
| c | 767 | 17 | 1.1 | 327 | 2 | US-08-429-965-3 | Sequence 3, Appli |
| c | 768 | 17 | 1.1 | 327 | 2 | US-08-969-584-3 | Sequence 3, Appli |
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| c | 770 | 17 | 1.1 | 327 | 2 | US-08-969-249A-3 | Sequence 3, Appli |
| c | 771 | 17 | 1.1 | 327 | 3 | US-08-969-378-3 | Sequence 3, Appli |
| c | 772 | 17 | 1.1 | 327 | 4 | US-09-136-594-3 | Sequence 3, Appli |
| c | 773 | 17 | 1.1 | 327 | 4 | US-09-137-134-3 | Sequence 3, Appli |
| c | 774 | 17 | 1.1 | 327 | 4 | US-09-417-797-3 | Sequence 3, Appli |
| c | 775 | 17 | 1.1 | 327 | 4 | US-09-416-434-3 | Sequence 3, Appli |
| c | 776 | 17 | 1.1 | 353 | 4 | US-09-299-495F-20 | Sequence 20, Appl |
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| c | 778 | 17 | 1.1 | 447 | 4 | US-09-222-575-61 | Sequence 61, Appl |
| c | 779 | 17 | 1.1 | 505 | 4 | US-09-222-575-59 | Sequence 59, Appl |
| c | 780 | 17 | 1.1 | 551 | 4 | US-09-222-575-142 | Sequence 142, App |
| c | 781 | 17 | 1.1 | 585 | 2 | US-08-702-105A-28 | Sequence 28, Appl |
| c | 782 | 17 | 1.1 | 585 | 2 | US-08-702-105A-30 | Sequence 30, Appl |
| c | 783 | 17 | 1.1 | 585 | 3 | US-08-702-110A-28 | Sequence 28, Appl |
| c | 784 | 17 | 1.1 | 585 | 3 | US-08-702-110A-30 | Sequence 30, Appl |
| c | 785 | 17 | 1.1 | 585 | 4 | US-09-325-571-28 | Sequence 28, Appl |
| c | 786 | 17 | 1.1 | 585 | 4 | US-09-325-571-30 | Sequence 30, Appl |
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| c | 798 | 17 | 1.1 | 860 | 3 | US-09-248-335-41 | Sequence 41, Appl |
| c | 799 | 17 | 1.1 | 900 | 4 | US-09-589-927-9 | Sequence 9, Appli |
| c | 800 | 17 | 1.1 | 900 | 4 | US-09-277-665-9 | Sequence 9, Appli |
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| c | 802 | 17 | 1.1 | 961 | 6 | 5219739-16 | Patent No. 5219739 |
| c | 803 | 17 | 1.1 | 966 | 1 | US-08-514-014-7 | Sequence 7, Appli |
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| c | 806 | 17 | 1.1 | 981 | 3 | US-08-816-977-36 | Sequence 36, Appl |
| c | 807 | 17 | 1.1 | 990 | 3 | US-08-816-977-38 | Sequence 38, Appl |
| | 808 | 17 | 1.1 | 1001 | 4 | US-09-641-638-175 | Sequence 175, App |
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| c | 810 | 17 | 1.1 | 1146 | 4 | US-09-609-161B-21 | Sequence 21, Appl |
| | 811 | 17 | 1.1 | 1210 | 4 | US-09-560-639-12 | Sequence 12, Appl |
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| c | 813 | 17 | 1.1 | 1354 | 1 | US-08-514-014-9 | Sequence 9, Appli |
| c | 814 | 17 | 1.1 | 1354 | 2 | US-08-833-823-9 | Sequence 9, Appli |
| | 815 | 17 | 1.1 | 1357 | 4 | US-09-560-639-5 | Sequence 5, Appli |
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| | 818 | 17 | 1.1 | 1383 | 3 | US-08-618-651A-7 | Sequence 7, Appli |
| | 819 | 17 | 1.1 | 1383 | 4 | US-09-215-252-6 | Sequence 6, Appli |
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| | 823 | 17 | 1.1 | 1426 | 4 | US-09-040-958-1 | Sequence 1, Appli |
| c | 824 | 17 | 1.1 | 1518 | 4 | US-09-257-581-6 | Sequence 6, Appli |
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| | 828 | 17 | 1.1 | 1680 | 4 | US-09-560-639-10 | Sequence 10, Appl |
| | 829 | 17 | 1.1 | 1693 | 4 | US-09-661-711A-1 | Sequence 1, Appli |
| | 830 | 17 | 1.1 | 1698 | 4 | US-09-661-711A-17 | Sequence 17, Appl |

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| c | 836 | 17 | 1.1 | 1843 | 5 | PCT-US95-03323A-1 | Sequence 1, Appli |
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| | 850 | 17 | 1.1 | 2369 | 4 | US-09-149-476-309 | Sequence 309, App |
| c | 851 | 17 | 1.1 | 2699 | 4 | US-09-460-145-3 | Sequence 3, Appli |
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| c | 856 | 17 | 1.1 | 3218 | 3 | US-09-434-065-1 | Sequence 1, Appli |
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| c | 860 | 17 | 1.1 | 3234 | 2 | US-08-346-128-31 | Sequence 31, Appl |
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| | 891 | 16 | 1.1 | 38 | 2 | US-08-857-946-106 | Sequence 106, App |
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| c | 897 | 16 | 1.1 | 51 | 4 | US-09-529-279-44 | Sequence 44, Appl |
| | 898 | 16 | 1.1 | 57 | 4 | US-08-796-101-183 | Sequence 183, App |
| | 899 | 16 | 1.1 | 57 | 4 | US-09-449-218D-27 | Sequence 27, Appl |
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| c | 902 | 16 | 1.1 | 93 | 4 | US-08-556-978B-87 | Sequence 87, Appl |
| | 903 | 16 | 1.1 | 93 | 4 | US-08-556-978B-88 | Sequence 88, Appl |
| | 904 | 16 | 1.1 | 165 | 1 | US-08-209-747-9 | Sequence 9, Appli |
| | 905 | 16 | 1.1 | 165 | 1 | US-08-458-298-9 | Sequence 9, Appli |
| c | 906 | 16 | 1.1 | 183 | 2 | US-08-611-757-42 | Sequence 42, Appl |
| c | 907 | 16 | 1.1 | 183 | 5 | PCT-US95-05980-42 | Sequence 42, Appl |
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| | 913 | 16 | 1.1 | 378 | 4 | US-08-776-971-28 | Sequence 28, Appl |
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| | 915 | 16 | 1.1 | 434 | 3 | US-08-513-974B-365 | Sequence 365, App |
| | 916 | 16 | 1.1 | 434 | 4 | US-08-776-971-105 | Sequence 105, App |
| | 917 | 16 | 1.1 | 514 | 4 | US-09-370-838-282 | Sequence 282, App |
| c | 918 | 16 | 1.1 | 537 | 4 | US-09-446-959-9 | Sequence 9, Appli |
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| | 923 | 16 | 1.1 | 633 | 5 | PCT-US95-05523-1 | Sequence 1, Appli |
| c | 924 | 16 | 1.1 | 641 | 2 | US-08-522-421-6 | Sequence 6, Appli |
| | 925 | 16 | 1.1 | 718 | 4 | US-08-961-527-295 | Sequence 295, App |
| c | 926 | 16 | 1.1 | 730 | 1 | US-08-359-696-1 | Sequence 1, Appli |
| c | 927 | 16 | 1.1 | 790 | 6 | 5194596-8 | Patent No. 5194596 |
| | 928 | 16 | 1.1 | 801 | 4 | US-08-998-416-449 | Sequence 449, App |
| c | 929 | 16 | 1.1 | 853 | 2 | US-08-695-736-2 | Sequence 2, Appli |
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| c | 941 | 16 | 1.1 | 1242 | 4 | US-09-134-001C-2138 | Sequence 2138, Ap |
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| | 945 | 16 | 1.1 | 1300 | 4 | US-08-795-876-36 | Sequence 36, Appl |
| c | 946 | 16 | 1.1 | 1300 | 4 | US-08-795-876-37 | Sequence 37, Appl |
| | 947 | 16 | 1.1 | 1333 | 4 | US-09-247-155-77 | Sequence 77, Appl |
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| c | 952 | 16 | 1.1 | 1568 | 4 | US-09-529-279-42 | Sequence 42, Appl |
| | 953 | 16 | 1.1 | 1599 | 1 | US-08-288-405A-9 | Sequence 9, Appli |
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| | 959 | 16 | 1.1 | 1869 | 3 | US-08-934-494-1 | Sequence 1, Appli |
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| c | 961 | 16 | 1.1 | 1869 | 3 | US-09-305-381-1 | Sequence 1, Appli |
| | 962 | 16 | 1.1 | 1869 | 4 | US-09-143-707-1 | Sequence 1, Appli |
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| | 964 | 16 | 1.1 | 1869 | 4 | US-09-511-133-1 | Sequence 1, Appli |
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| c | 972 | 16 | 1.1 | 1889 | 2 | US-09-227-420-2 | Sequence 2, Appli |
| | 973 | 16 | 1.1 | 1896 | 1 | US-08-198-446B-8 | Sequence 8, Appli |
| | 974 | 16 | 1.1 | 1896 | 2 | US-08-870-693-8 | Sequence 8, Appli |
| c | 975 | 16 | 1.1 | 1948 | 4 | US-09-352-990-1 | Sequence 1, Appli |
| c | 976 | 16 | 1.1 | 2338 | 1 | US-08-425-069-1 | Sequence 1, Appli |

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| 982 | 16 | 1.1 | 2360 | 2 | US-08-483-924-1 | Sequence 1, Appli |
| 983 | 16 | 1.1 | 2360 | 5 | PCT-US93-06160-1 | Sequence 1, Appli |
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| c 989 | 16 | 1.1 | 2816 | 1 | US-08-785-241-1 | Sequence 1, Appli |
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| c 993 | 16 | 1.1 | 2830 | 5 | PCT-US93-04102-1 | Sequence 1, Appli |
| c 994 | 16 | 1.1 | 2848 | 3 | US-08-539-205A-3 | Sequence 3, Appli |
| c 995 | 16 | 1.1 | 2885 | 3 | US-08-948-705-2 | Sequence 2, Appli |
| 996 | 16 | 1.1 | 2890 | 1 | US-07-928-464-1 | Sequence 1, Appli |
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| 999 | 16 | 1.1 | 3033 | 1 | US-08-003-311B-1 | Sequence 1, Appli |
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ALIGNMENTS

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RESULT 1
US-07-811-048-9
; Sequence 9, Application US/07811048
; Patent No. 5264357
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    TITLE OF INVENTION:  Nucleic Acid and Methods for the Synthesis of No. 5264357el Fu
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/811,048
;      FILING DATE:  19911219
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/738171
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/859107
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US86/01177
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/083757
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Robert H.
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  330p1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1489
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2116 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-811-048-9

  Query Match             90.8%;  Score 1356;  DB 1;  Length 2116;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
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Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
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Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

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Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
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Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
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RESULT 2
US-08-087-007-2
; Sequence 2, Application US/08087007
; Patent No. 5705732
; Patent No. 5705732 5684223
;  GENERAL INFORMATION:
;    APPLICANT:  Sims, Peter J.
;    APPLICANT:  Bothwell, Alfred L.M.
;    APPLICANT:  Elliott, Eileen A.
;    APPLICANT:  Flavell, Richard A.
;    APPLICANT:  Madri, Joseph
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Squinto, Stephen
;    TITLE OF INVENTION:  Universal Donor Cells
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kilpatrick & Cody
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/087,007
;      FILING DATE:  19930701
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  OMRF135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-815-6500
;      TELEFAX:  404-815-6555
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2847 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
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;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank HUMDAF; HUMDAFC1
;      CLONE:  Human DAF cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..819
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US-08-087-007-2

  Query Match             80.6%;  Score 1203;  DB 1;  Length 2847;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1353;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
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RESULT 3
US-08-483-433-2
; Sequence 2, Application US/08483433
; Patent No. 6100443
;  GENERAL INFORMATION:
;    APPLICANT:  Sims et al.
;    TITLE OF INVENTION:  Universal Donor Cells
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,433
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/087,007
;      FILING DATE:  July 1, 1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/906,394
;      FILING DATE:  June 29, 1992
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  OMRF135cip2 div
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-873-8794
;      TELEFAX:  404-873-9794
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2847 base pairs
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Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
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Db    995 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAC 1054

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   1055 CTGCCTTAAGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 1114

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1115 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 1174

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1175 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 1234

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1235 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 1294

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1295 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 1354

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1355 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 1414

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1415 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 1474

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1475 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 1534

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1535 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 1594

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1595 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1654

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1655 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1714

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1715 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1774

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1775 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1834

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1835 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1894

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1895 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1954

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1955 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 2014

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2015 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 2074

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||||||||||
Db   2075 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 2110


RESULT 4
PCT-US92-05920-2
; Sequence 2, Application PC/TUS9205920
;  GENERAL INFORMATION:
;    APPLICANT:  Sims, Peter J.
;    APPLICANT:  Bothwell, Alfred L.M.
;    APPLICANT:  Elliott, Eileen A.
;    APPLICANT:  Flavell, Richard A.
;    APPLICANT:  Madri, Joseph
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Squinto, Stephen
;    TITLE OF INVENTION:  Universal Donor Cells
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kilpatrick & Cody
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05920
;      FILING DATE:  19920714
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  OMRF135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-815-6500
;      TELEFAX:  404-815-6555
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2847 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank HUMDAF; HUMDAFC1
;      CLONE:  Human DAF cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..819
;      OTHER INFORMATION:  /note= "HUMDAFC1 (Promotor and 5'
;      OTHER INFORMATION:  end of Exon 1, genomic sequence)"
PCT-US92-05920-2

  Query Match             80.6%;  Score 1203;  DB 5;  Length 2847;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1353;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    755 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 814

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    815 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 874

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    875 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 934

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    935 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 994

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    995 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAC 1054

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          |||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db   1055 CTGCCTTAAGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 1114

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1115 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 1174

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
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Db   1175 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 1234

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
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Db    1235 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 1294

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737

Db    1295 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 1354

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797

Db    1355 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 1414

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857

Db    1415 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 1474

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917

Db    1475 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 1534

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977

Db    1535 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 1594

Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037

Db    1595 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1654

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097

Db    1655 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1714

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157

Db    1715 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1774

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217

Db    1775 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1834

Qy    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277

Db    1835 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1894

Qy    1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337

Db    1895 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1954

Qy    1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397

Db    1955 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 2014

Qy    1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457

Db    2015 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 2074

Qy    1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493

Db    2075 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 2110


RESULT 5
US-08-458-084-1
; Sequence 1, Application US/08458084
; Patent No. 5624837
;  GENERAL INFORMATION:
;    APPLICANT:  Fodor, William L
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Squinto, Stephen P
;    TITLE OF INVENTION:  Chimeric Complement
;    TITLE OF INVENTION:  Inhibitor Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,084
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
US-08-458-084-1

  Query Match             80.0%;  Score 1195;  DB 1;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205

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Qy     206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265

Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325

Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385

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Qy     446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505

Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
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Db      361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy      566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy      626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy      686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy      746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy      806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy      866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy      926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy      986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

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Db     1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy     1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
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Db     1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy     1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
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Db     1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy     1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
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Db     1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy     1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
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Db     1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy     1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db     1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
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RESULT 6
US-08-205-508-1
; Sequence 1, Application US/08205508
; Patent No. 5627264
;  GENERAL INFORMATION:
;    APPLICANT:  Fodor, William L
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Squinto, Stephen P
;    TITLE OF INVENTION:  Chimeric Complement
;    TITLE OF INVENTION:  Inhibitor Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/205,508
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
US-08-205-508-1

  Query Match             80.0%;  Score 1195;  DB 1;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
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Db        1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy      266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy      326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
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Db      181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy      386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
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Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
          ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy    566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
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Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
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Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
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Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy   1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy   1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy   1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy   1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy   1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
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Qy   1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
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Db   1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy   1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy   1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db   1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
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RESULT 7
US-08-278-630A-10
; Sequence 10, Application US/08278630A
; Patent No. 5643770
;  GENERAL INFORMATION:
;    APPLICANT:  Mason, James M.
;    APPLICANT:  Squinto, Stephen P.
;    TITLE OF INVENTION:  Retroviral Vector Particles
;    TITLE OF INVENTION:  Expressing Complement Inhibitor Activity
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/278,630A
;      FILING DATE:  July 21, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
US-08-278-630A-10

  Query Match             80.0%;  Score 1195;  DB 1;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
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Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy     206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120
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Qy    266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
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Db    121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy    326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy    386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
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Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
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Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
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Qy    566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
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Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
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Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
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Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
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Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
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Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
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Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
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Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
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Db    841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy   1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
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Db    901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy   1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
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Db    961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy   1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
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Db   1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy   1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy   1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
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Qy   1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
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Db   1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

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Db   1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy   1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||
Db   1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
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RESULT 8
PCT-US95-02945-1
; Sequence 1, Application PC/TUS9502945
;  GENERAL INFORMATION:
;    APPLICANT:  Fodor, William L
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Squinto, Stephen P
;    TITLE OF INVENTION:  Chimeric Complement
;    TITLE OF INVENTION:  Inhibitor Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02945
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/205,508
;      FILING DATE:  3-MAR-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-120PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
PCT-US95-02945-1
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  Query Match             80.0%;  Score 1195;  DB 5;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
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Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy     206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
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Qy     326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
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Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
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Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
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Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
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Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
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Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
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Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
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Qy     746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
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Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
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Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
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Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy    1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy    1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348


RESULT 9
US-07-811-048-10
; Sequence 10, Application US/07811048
; Patent No. 5264357
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    TITLE OF INVENTION:  Nucleic Acid and Methods for the Synthesis of No. 5264357el
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/811,048
;      FILING DATE:  19911219
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/738171
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/859107
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US86/01177
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/083757
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Robert H.
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  330p1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1489
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2234 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-811-048-10

  Query Match             76.6%;  Score 1143;  DB 1;  Length 2234;
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  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC  64

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy    1278 TGG 1280
           |||
Db    1145 TGG 1147


RESULT 10
US-09-475-460A-31
; Sequence 31, Application US/09475460A
; Patent No. 6316253
; GENERAL INFORMATION:
;  APPLICANT:  Scott, Elizabeth
;  APPLICANT:  Innis, Michael
;  TITLE OF INVENTION:  EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE:  1527.003
;  CURRENT APPLICATION NUMBER: US/09/475,460A
;  CURRENT FILING DATE:  1999-12-30
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1848
;   TYPE: DNA
;   ORGANISM: CAB2
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1839)
US-09-475-460A-31

  Query Match            65.0%;  Score 970;  DB 4;  Length 1848;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  970;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     300 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 929

Qy     360 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 989

Qy     420 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 1049

Qy     480 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 1109

Qy     540 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 1169

Qy     600 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1170 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 1229

Qy     660 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 1289

Qy     720 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1290 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 1349

Qy     780 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1350 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 1409
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Qy    840 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 1469

Qy    900 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 1529

Qy    960 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1530 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1589

Qy   1020 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1649

Qy   1080 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1709

Qy   1140 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1769

Qy   1200 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1829

Qy   1260 TACTACCCGT 1269
          ||||||||||
Db   1830 TACTACCCGT 1839


RESULT 11
US-09-748-061A-31
; Sequence 31, Application US/09748061A
; Patent No. 6451539
; GENERAL INFORMATION:
;  APPLICANT: Scott, Elizabeth
;  APPLICANT:  Innis, Michael
;  TITLE OF INVENTION: EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: PP01527.101 / 2302-1527.10
;  CURRENT APPLICATION NUMBER: US/09/748,061A
;  CURRENT FILING DATE:  2000-12-22
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1848
;   TYPE: DNA
;   ORGANISM: CAB2
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1839)
US-09-748-061A-31

  Query Match            65.0%;  Score 970;  DB 4;  Length 1848;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  970;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    300 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 359
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Db    870 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 929

Qy    360 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 419
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Db    930 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 989

Qy    420 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 479
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 1049

Qy    480 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 539
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 1109

Qy    540 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 1169

Qy    600 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 659
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 1229

Qy    660 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 719
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 1289

Qy    720 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 779
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 1349

Qy    780 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 839
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 1409

Qy    840 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 899
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 1469

Qy    900 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 959
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 1529

Qy    960 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1019
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1530 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1589

Qy   1020 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1079
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1649

Qy   1080 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1139
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1709

Qy   1140 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1769

Qy   1200 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1829

Qy   1260 TACTACCCGT 1269
          ||||||||||
Db   1830 TACTACCCGT 1839


RESULT 12
US-08-435-149-17
; Sequence 17, Application US/08435149
; Patent No. 5866402
;  GENERAL INFORMATION:
;    APPLICANT:  INNIS, MICHAEL A.
;    APPLICANT:  ZAROR, ISABEL
;    APPLICANT:  CREASEY, ABLA A.
;    TITLE OF INVENTION:  CHIMERIC MCP AND DAF PROTEINS WITH CELL
;    TITLE OF INVENTION:  SURFACE LOCALIZING DOMAIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION
;      STREET:  INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
```

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;       COUNTRY:  U.S.A.
;       ZIP:  94662-8097
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/435,149
;       FILING DATE:  05-MAY-1995
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SAVEREIDE, PAUL B.
;       REGISTRATION NUMBER:  36,914
;       REFERENCE/DOCKET NUMBER:  0989.001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (510) 601-2585
;       TELEFAX:  (510) 655-3542
;       TELEX:  N/A
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1878 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-435-149-17

  Query Match             65.0%;  Score 970;  DB 2;  Length 1878;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  970;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     300 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     906 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 965

Qy     360 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     966 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 1025

Qy     420 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 479
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1026 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 1085

Qy     480 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 539
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1086 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 1145

Qy     540 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 599
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1146 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 1205

Qy     600 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 659
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1206 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 1265

Qy     660 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 719
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1266 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 1325

Qy     720 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 779
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1326 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 1385

Qy     780 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 839
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1386 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 1445

Qy     840 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 899
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1446 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 1505

Qy     900 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 959
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1506 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 1565

Qy     960 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1019
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1566 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1625

Qy    1020 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1079
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1626 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1685

Qy    1080 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1139
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1686 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1745

Qy    1140 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1746 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1805

Qy    1200 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1806 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1865

Qy    1260 TACTACCCGT 1269
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Db    1866 TACTACCCGT 1875


RESULT 13
US-08-310-416A-12
; Sequence 12, Application US/08310416A
; Patent No. 5679546
;  GENERAL INFORMATION:
;    APPLICANT:  Jone-Long Ko et al.
;    TITLE OF INVENTION:  CHIMERIC PROTEINS WHICH BLOCK
;    TITLE OF INVENTION:  COMPLEMENT ACTIVATION
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,416A
;      FILING DATE:  22-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul T. Clark
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06180/005001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  969 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-310-416A-12

  Query Match             54.7%;  Score 816;  DB 1;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  816;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy    454 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 513
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Db    154 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 213

Qy    514 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 273

Qy    574 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 333

Qy    634 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 393

Qy    694 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 453

Qy    754 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 513

Qy    814 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 573

Qy    874 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 633

Qy    934 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 693

Qy    994 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 753

Qy   1054 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 813

Qy   1114 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 873

Qy   1174 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 933

Qy   1234 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGT 1269
          |||||||||||||||||||||||||||||||||||
Db    934 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGT 969
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RESULT 14
US-08-888-171-12
; Sequence 12, Application US/08888171
; Patent No. 5851528
;  GENERAL INFORMATION:
;    APPLICANT:  Jone-Long, Ko
;    APPLICANT:  Higgins, Paul J.
;    APPLICANT:  Yeh, C. Grace
;    TITLE OF INVENTION:  METHODS OF INHIBITING COMPLEMENT
;    TITLE OF INVENTION:  ACTIVATION
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,171
;      FILING DATE:  03-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/310,416
;      FILING DATE:  22-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06180/005002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-507
;      TELEFAX:  617/542-890
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  969 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-888-171-12

  Query Match             54.7%;  Score 816;  DB 2;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  816;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    454 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 513
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Db    154 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 213

Qy    514 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    214 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 273

Qy    574 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 333

Qy    634 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    334 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 393

Qy    694 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 453

Qy    754 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    454 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 513

Qy    814 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 873
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Db    514 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 573

Qy    874 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    574 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 633

Qy    934 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 693

Qy    994 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 1053
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Db    694 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 753

Qy   1054 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 1113
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Db    754 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 813

Qy   1114 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 1173
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 873

Qy   1174 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1233
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Db    874 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 933

Qy   1234 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGT 1269
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Db    934 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGT 969
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RESULT 15
US-08-310-416A-19
; Sequence 19, Application US/08310416A
; Patent No. 5679546
; GENERAL INFORMATION:
; APPLICANT: Jone-Long Ko et al.
; TITLE OF INVENTION: CHIMERIC PROTEINS WHICH BLOCK
; TITLE OF INVENTION: COMPLEMENT ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/310,416A
; FILING DATE: 22-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06180/005001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 860 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-310-416A-19

Query Match 47.4%; Score 707; DB 1; Length 860;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 857; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    197 CCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCC 256
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Db      1 CCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCC 60

Qy    257 GGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCC 316
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCC 120

Qy    317 CAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTG 376
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Db    121 CAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTG 180

Qy    377 TAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGA 436
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Db    181 TAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGA 240

Qy    437 TCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGG 496
          |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    241 CCTGCCTTAAGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGG 300

Qy    497 TGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTC 556
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTC 360

Qy    557 CAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTAT 616
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTAT 420

Qy    617 CACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAA 676
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Db    421 CACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAA 480

Qy    677 AGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCA 736
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Db    481 AGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCA 540

Qy    737 TATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGA 796
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Db    541 TATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGA 600

Qy    797 CTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGT 856
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Db    601 CTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGT 660

Qy    857 GCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAAC 916
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Db    661 GCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAAC 720

Qy    917 GTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGA 976
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGA 780

Qy    977 TTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCAC 1036
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Db    781 TTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCAC 840

Qy   1037 CACCTGAATGCAGAGGAAAA 1056
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Db    841 CACCTGAATGCAGAGGAAAA 860
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Job time : 83.5736 secs

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 05:25:37 ; Search time 84.721 Seconds
(without alignments)
9897.518 Million cell updates/sec

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Perfect score: 1493
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 442118 seqs, 280819700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 884236

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| c | 225 | 21 | 1.4 | 2088 | 10 | US-09-681-442-13 | Sequence 13, Appl |
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| c | 230 | 21 | 1.4 | 2094 | 10 | US-09-795-847-17 | Sequence 17, Appl |
| c | 231 | 21 | 1.4 | 2094 | 10 | US-09-795-847-19 | Sequence 19, Appl |
| c | 232 | 21 | 1.4 | 2094 | 10 | US-09-794-743-15 | Sequence 15, Appl |
| c | 233 | 21 | 1.4 | 2094 | 10 | US-09-794-743-17 | Sequence 17, Appl |
| c | 234 | 21 | 1.4 | 2094 | 10 | US-09-794-743-19 | Sequence 19, Appl |
| c | 235 | 21 | 1.4 | 2094 | 10 | US-09-794-748-15 | Sequence 15, Appl |
| c | 236 | 21 | 1.4 | 2094 | 10 | US-09-794-748-17 | Sequence 17, Appl |
| c | 237 | 21 | 1.4 | 2094 | 10 | US-09-794-748-19 | Sequence 19, Appl |
| c | 238 | 21 | 1.4 | 2094 | 10 | US-09-794-925-15 | Sequence 15, Appl |

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| c | 239 | 21 | 1.4 | 2094 | 10 | US-09-794-925-17 | Sequence 17, Appl |
| c | 240 | 21 | 1.4 | 2094 | 10 | US-09-794-925-19 | Sequence 19, Appl |
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| c | 242 | 21 | 1.4 | 2094 | 10 | US-09-681-442-17 | Sequence 17, Appl |
| c | 243 | 21 | 1.4 | 2094 | 10 | US-09-681-442-19 | Sequence 19, Appl |
| c | 244 | 21 | 1.4 | 2253 | 10 | US-09-794-927-56 | Sequence 56, Appl |
| c | 245 | 21 | 1.4 | 2253 | 10 | US-09-795-847-56 | Sequence 56, Appl |
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| c | 263 | 21 | 1.4 | 2310 | 10 | US-09-149-718-5 | Sequence 5, Appli |
| c | 264 | 21 | 1.4 | 2313 | 9 | US-09-785-215-1 | Sequence 1, Appli |
| c | 265 | 21 | 1.4 | 2316 | 10 | US-09-794-927-58 | Sequence 58, Appl |
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| c | 268 | 21 | 1.4 | 2316 | 10 | US-09-794-748-58 | Sequence 58, Appl |
| c | 269 | 21 | 1.4 | 2316 | 10 | US-09-794-925-58 | Sequence 58, Appl |
| c | 270 | 21 | 1.4 | 2316 | 10 | US-09-681-442-58 | Sequence 58, Appl |
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| c | 272 | 21 | 1.4 | 2735 | 10 | US-09-874-923-101 | Sequence 101, App |
| c | 273 | 21 | 1.4 | 2781 | 9 | US-09-991-496-125 | Sequence 125, App |
| c | 274 | 21 | 1.4 | 2868 | 9 | US-09-991-496-123 | Sequence 123, App |
| c | 275 | 21 | 1.4 | 3012 | 9 | US-09-991-496-94 | Sequence 94, Appl |
| c | 276 | 21 | 1.4 | 3012 | 10 | US-09-874-923-94 | Sequence 94, Appl |
| c | 277 | 21 | 1.4 | 3354 | 10 | US-09-794-975-10 | Sequence 10, Appl |
| c | 278 | 21 | 1.4 | 4929 | 9 | US-09-991-496-98 | Sequence 98, Appl |
| c | 279 | 21 | 1.4 | 4929 | 10 | US-09-874-923-98 | Sequence 98, Appl |
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| c | 281 | 21 | 1.4 | 6485 | 12 | US-10-044-090-290 | Sequence 290, App |
| c | 282 | 21 | 1.4 | 23770 | 9 | US-10-035-637-8 | Sequence 8, Appli |
| | 283 | 21 | 1.4 | 62944 | 10 | US-09-954-456-2257 | Sequence 2257, Ap |
| c | 284 | 21 | 1.4 | 145831 | 10 | US-09-969-708-79 | Sequence 79, Appl |
| c | 285 | 21 | 1.4 | 145831 | 10 | US-09-954-456-2116 | Sequence 2116, Ap |
| c | 286 | 21 | 1.4 | 167343 | 10 | US-09-962-436-281 | Sequence 281, App |
| c | 287 | 21 | 1.4 | 167343 | 10 | US-09-964-824A-273 | Sequence 273, App |
| c | 288 | 20 | 1.3 | 21 | 10 | US-09-828-034-11 | Sequence 11, Appl |
| c | 289 | 20 | 1.3 | 21 | 10 | US-09-828-034-31 | Sequence 31, Appl |
| | 290 | 20 | 1.3 | 72 | 10 | US-09-748-264A-6 | Sequence 6, Appli |
| c | 291 | 20 | 1.3 | 96 | 10 | US-09-969-373-1233 | Sequence 1233, Ap |
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| c | 293 | 20 | 1.3 | 126 | 10 | US-09-864-761-29287 | Sequence 29287, A |
| | 294 | 20 | 1.3 | 158 | 10 | US-09-864-761-17079 | Sequence 17079, A |
| | 295 | 20 | 1.3 | 162 | 10 | US-09-864-761-17565 | Sequence 17565, A |
| | 296 | 20 | 1.3 | 162 | 10 | US-09-864-761-25801 | Sequence 25801, A |
| | 297 | 20 | 1.3 | 196 | 10 | US-09-864-761-20007 | Sequence 20007, A |
| c | 298 | 20 | 1.3 | 209 | 9 | US-09-948-049-3 | Sequence 3, Appli |
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| | 300 | 20 | 1.3 | 249 | 10 | US-09-864-761-16846 | Sequence 16846, A |
| c | 301 | 20 | 1.3 | 267 | 10 | US-09-878-574-7079 | Sequence 7079, Ap |
| c | 302 | 20 | 1.3 | 301 | 10 | US-09-825-301-74 | Sequence 74, Appl |
| c | 303 | 20 | 1.3 | 358 | 10 | US-09-770-791-585 | Sequence 585, App |
| c | 304 | 20 | 1.3 | 380 | 10 | US-09-878-574-1843 | Sequence 1843, Ap |
| | 305 | 20 | 1.3 | 387 | 10 | US-09-864-761-4536 | Sequence 4536, Ap |
| | 306 | 20 | 1.3 | 401 | 10 | US-09-864-761-3936 | Sequence 3936, Ap |
| c | 307 | 20 | 1.3 | 403 | 10 | US-09-960-352-3169 | Sequence 3169, Ap |
| | 308 | 20 | 1.3 | 428 | 10 | US-09-864-761-5767 | Sequence 5767, Ap |
| | 309 | 20 | 1.3 | 446 | 10 | US-09-864-761-20699 | Sequence 20699, A |
| | 310 | 20 | 1.3 | 461 | 10 | US-09-864-761-259 | Sequence 259, App |
| c | 311 | 20 | 1.3 | 464 | 10 | US-09-833-790-30 | Sequence 30, Appl |
| | 312 | 20 | 1.3 | 467 | 10 | US-09-864-761-1238 | Sequence 1238, Ap |
| | 313 | 20 | 1.3 | 476 | 10 | US-09-864-761-6 | Sequence 6, Appli |
| c | 314 | 20 | 1.3 | 484 | 10 | US-09-864-761-2491 | Sequence 2491, Ap |
| c | 315 | 20 | 1.3 | 491 | 9 | US-09-854-133-343 | Sequence 343, App |
| | 316 | 20 | 1.3 | 491 | 10 | US-09-864-761-781 | Sequence 781, App |
| c | 317 | 20 | 1.3 | 491 | 10 | US-09-738-973-343 | Sequence 343, App |
| c | 318 | 20 | 1.3 | 524 | 9 | US-10-090-035-17 | Sequence 17, Appl |
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| c | 320 | 20 | 1.3 | 544 | 10 | US-09-864-761-12721 | Sequence 12721, A |
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| c | 322 | 20 | 1.3 | 580 | 9 | US-10-090-035-7 | Sequence 7, Appli |
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| c | 327 | 20 | 1.3 | 1002 | 12 | US-10-062-254-203 | Sequence 203, App |
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| c | 329 | 20 | 1.3 | 1008 | 9 | US-09-850-258-3 | Sequence 3, Appli |
| c | 330 | 20 | 1.3 | 1008 | 10 | US-09-850-260-1 | Sequence 1, Appli |
| c | 331 | 20 | 1.3 | 1008 | 10 | US-09-850-260-3 | Sequence 3, Appli |
| | 332 | 20 | 1.3 | 1075 | 10 | US-09-864-761-19241 | Sequence 19241, A |
| c | 333 | 20 | 1.3 | 1203 | 9 | US-09-879-312-1 | Sequence 1, Appli |
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| c | 335 | 20 | 1.3 | 1259 | 9 | US-09-991-209-43 | Sequence 43, Appl |
| | 336 | 20 | 1.3 | 1368 | 9 | US-09-938-842A-178 | Sequence 178, App |
| | 337 | 20 | 1.3 | 1403 | 10 | US-09-864-761-2513 | Sequence 2513, Ap |
| | 338 | 20 | 1.3 | 1561 | 10 | US-09-765-272-121 | Sequence 121, App |
| c | 339 | 20 | 1.3 | 1602 | 10 | US-09-833-790-417 | Sequence 417, App |
| c | 340 | 20 | 1.3 | 1635 | 10 | US-09-864-761-20241 | Sequence 20241, A |
| c | 341 | 20 | 1.3 | 1722 | 12 | US-10-062-254-271 | Sequence 271, App |
| c | 342 | 20 | 1.3 | 1817 | 10 | US-09-822-849A-83 | Sequence 83, Appl |
| c | 343 | 20 | 1.3 | 1935 | 9 | US-09-778-510-21 | Sequence 21, Appl |
| c | 344 | 20 | 1.3 | 1935 | 9 | US-09-778-187B-3 | Sequence 3, Appli |
| c | 345 | 20 | 1.3 | 1966 | 9 | US-09-764-868-152 | Sequence 152, App |
| c | 346 | 20 | 1.3 | 1973 | 10 | US-09-864-761-3471 | Sequence 3471, Ap |
| c | 347 | 20 | 1.3 | 2209 | 10 | US-09-925-301-494 | Sequence 494, App |
| c | 348 | 20 | 1.3 | 2433 | 10 | US-09-944-807-3 | Sequence 3, Appli |
| | 349 | 20 | 1.3 | 2453 | 12 | US-10-005-858-1 | Sequence 1, Appli |
| | 350 | 20 | 1.3 | 2725 | 10 | US-09-962-436-40 | Sequence 40, Appl |
| c | 351 | 20 | 1.3 | 2732 | 10 | US-09-925-297-199 | Sequence 199, App |
| | 352 | 20 | 1.3 | 2811 | 9 | US-09-759-130B-303 | Sequence 303, App |
| | 353 | 20 | 1.3 | 2834 | 10 | US-09-954-456-286 | Sequence 286, App |
| | 354 | 20 | 1.3 | 2834 | 10 | US-09-954-456-951 | Sequence 951, App |
| | 355 | 20 | 1.3 | 2834 | 10 | US-09-954-456-1603 | Sequence 1603, Ap |
| c | 356 | 20 | 1.3 | 2990 | 9 | US-09-854-133-731 | Sequence 731, App |
| | 357 | 20 | 1.3 | 3121 | 10 | US-09-765-272-117 | Sequence 117, App |
| c | 358 | 20 | 1.3 | 3158 | 12 | US-10-078-929-187 | Sequence 187, App |
| | 359 | 20 | 1.3 | 3233 | 10 | US-09-864-761-21283 | Sequence 21283, A |
| c | 360 | 20 | 1.3 | 3630 | 10 | US-09-925-301-111 | Sequence 111, App |
| c | 361 | 20 | 1.3 | 3802 | 10 | US-09-853-386-46 | Sequence 46, Appl |
| c | 362 | 20 | 1.3 | 3802 | 10 | US-09-853-386-78 | Sequence 78, Appl |
| c | 363 | 20 | 1.3 | 4032 | 10 | US-09-970-921-5 | Sequence 5, Appli |
| c | 364 | 20 | 1.3 | 4236 | 8 | US-08-965-272-1 | Sequence 1, Appli |
| c | 365 | 20 | 1.3 | 4236 | 12 | US-10-121-882-1 | Sequence 1, Appli |
| c | 366 | 20 | 1.3 | 4773 | 9 | US-09-991-209-32 | Sequence 32, Appl |
| c | 367 | 20 | 1.3 | 4950 | 9 | US-09-991-209-34 | Sequence 34, Appl |
| c | 368 | 20 | 1.3 | 4965 | 9 | US-09-991-209-37 | Sequence 37, Appl |
| c | 369 | 20 | 1.3 | 4974 | 9 | US-09-991-209-35 | Sequence 35, Appl |
| | 370 | 20 | 1.3 | 5119 | 9 | US-09-887-540A-1 | Sequence 1, Appli |
| c | 371 | 20 | 1.3 | 5164 | 9 | US-09-991-209-36 | Sequence 36, Appl |
| c | 372 | 20 | 1.3 | 5277 | 9 | US-09-991-209-25 | Sequence 25, Appl |
| c | 373 | 20 | 1.3 | 5295 | 9 | US-09-991-209-38 | Sequence 38, Appl |
| c | 374 | 20 | 1.3 | 5327 | 9 | US-09-991-209-27 | Sequence 27, Appl |
| c | 375 | 20 | 1.3 | 5337 | 9 | US-09-991-209-19 | Sequence 19, Appl |
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| c | 377 | 20 | 1.3 | 5337 | 9 | US-09-991-209-31 | Sequence 31, Appl |
| c | 378 | 20 | 1.3 | 5338 | 9 | US-09-991-209-15 | Sequence 15, Appl |
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| c | 380 | 20 | 1.3 | 5345 | 9 | US-09-991-209-17 | Sequence 17, Appl |
| c | 381 | 20 | 1.3 | 5387 | 9 | US-09-991-209-41 | Sequence 41, Appl |
| c | 382 | 20 | 1.3 | 5395 | 9 | US-09-991-209-21 | Sequence 21, Appl |
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| c 386 | 20 | 1.3 | 9757 | 9 | US-10-126-912-7 | Sequence 7, Appli |
| c 387 | 20 | 1.3 | 9828 | 9 | US-10-126-912-1 | Sequence 1, Appli |
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| 389 | 20 | 1.3 | 15016 | 10 | US-09-880-107-3783 | Sequence 3783, Ap |
| 390 | 20 | 1.3 | 40433 | 10 | US-09-880-107-3327 | Sequence 3327, Ap |
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| 399 | 19 | 1.3 | 43 | 12 | US-10-043-142-4 | Sequence 4, Appli |
| c 400 | 19 | 1.3 | 53 | 9 | US-09-941-492-112 | Sequence 112, App |
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| 403 | 19 | 1.3 | 57 | 9 | US-10-020-436A-3 | Sequence 3, Appli |
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| 405 | 19 | 1.3 | 97 | 9 | US-09-902-941-738 | Sequence 738, App |
| 406 | 19 | 1.3 | 97 | 9 | US-09-849-626-738 | Sequence 738, App |
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| c 420 | 19 | 1.3 | 241 | 9 | US-10-076-622-316 | Sequence 316, App |
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| c 448 | 19 | 1.3 | 301 | 9 | US-09-895-814-275 | Sequence 275, App |
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| 464 | 19 | 1.3 | 325 | 9 | US-09-902-941-530 | Sequence 530, App |
| 465 | 19 | 1.3 | 325 | 9 | US-09-849-626-530 | Sequence 530, App |
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| 467 | 19 | 1.3 | 334 | 9 | US-09-736-457-534 | Sequence 534, App |
| 468 | 19 | 1.3 | 334 | 9 | US-09-902-941-534 | Sequence 534, App |
| 469 | 19 | 1.3 | 334 | 9 | US-09-849-626-534 | Sequence 534, App |
| c 470 | 19 | 1.3 | 336 | 10 | US-09-884-441-286 | Sequence 286, App |
| c 471 | 19 | 1.3 | 360 | 9 | US-10-025-380-399 | Sequence 399, App |
| c 472 | 19 | 1.3 | 360 | 10 | US-09-922-217-399 | Sequence 399, App |
| c 473 | 19 | 1.3 | 360 | 10 | US-09-833-263-399 | Sequence 399, App |
| 474 | 19 | 1.3 | 366 | 9 | US-09-736-457-542 | Sequence 542, App |
| 475 | 19 | 1.3 | 366 | 9 | US-09-902-941-542 | Sequence 542, App |
| 476 | 19 | 1.3 | 366 | 9 | US-09-849-626-542 | Sequence 542, App |
| 477 | 19 | 1.3 | 368 | 9 | US-09-796-692-6665 | Sequence 6665, Ap |
| 478 | 19 | 1.3 | 372 | 10 | US-09-878-574-1717 | Sequence 1717, Ap |
| c 479 | 19 | 1.3 | 372 | 10 | US-09-920-300A-127 | Sequence 127, App |
| c 480 | 19 | 1.3 | 372 | 12 | US-10-033-528-127 | Sequence 127, App |
| 481 | 19 | 1.3 | 376 | 10 | US-09-827-669-61 | Sequence 61, Appl |
| 482 | 19 | 1.3 | 381 | 10 | US-09-864-761-17104 | Sequence 17104, A |
| 483 | 19 | 1.3 | 381 | 10 | US-09-864-761-21181 | Sequence 21181, A |
| 484 | 19 | 1.3 | 387 | 9 | US-10-076-622-133 | Sequence 133, App |
| 485 | 19 | 1.3 | 387 | 10 | US-09-604-287A-133 | Sequence 133, App |
| 486 | 19 | 1.3 | 387 | 10 | US-09-339-338-133 | Sequence 133, App |
| 487 | 19 | 1.3 | 387 | 12 | US-10-007-805-133 | Sequence 133, App |
| c 488 | 19 | 1.3 | 396 | 9 | US-09-970-966-136 | Sequence 136, App |
| c 489 | 19 | 1.3 | 396 | 10 | US-09-825-294-136 | Sequence 136, App |
| c 490 | 19 | 1.3 | 414 | 10 | US-09-924-401-22 | Sequence 22, Appl |
| 491 | 19 | 1.3 | 415 | 10 | US-09-815-343-1510 | Sequence 1510, Ap |
| c 492 | 19 | 1.3 | 419 | 10 | US-09-878-574-4107 | Sequence 4107, Ap |
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| c 494 | 19 | 1.3 | 438 | 10 | US-09-815-343-573 | Sequence 573, App |
| c 495 | 19 | 1.3 | 447 | 9 | US-10-076-622-168 | Sequence 168, App |
| c 496 | 19 | 1.3 | 447 | 10 | US-09-770-444-750 | Sequence 750, App |
| c 497 | 19 | 1.3 | 447 | 10 | US-09-604-287A-168 | Sequence 168, App |
| c 498 | 19 | 1.3 | 447 | 10 | US-09-339-338-168 | Sequence 168, App |
| c 499 | 19 | 1.3 | 447 | 12 | US-10-007-805-168 | Sequence 168, App |
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| 503 | 19 | 1.3 | 453 | 9 | US-09-849-626-1661 | Sequence 1661, Ap |
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| c 505 | 19 | 1.3 | 468 | 9 | US-09-768-020-17 | Sequence 17, Appl |
| 506 | 19 | 1.3 | 470 | 10 | US-09-864-761-285 | Sequence 285, App |
| 507 | 19 | 1.3 | 477 | 9 | US-09-736-457-670 | Sequence 670, App |
| 508 | 19 | 1.3 | 477 | 9 | US-09-902-941-670 | Sequence 670, App |
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| 513 | 19 | 1.3 | 487 | 9 | US-09-849-626-1655 | Sequence 1655, Ap |
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| c 515 | 19 | 1.3 | 493 | 10 | US-09-604-287A-53 | Sequence 53, Appl |
| c 516 | 19 | 1.3 | 493 | 10 | US-09-339-338-53 | Sequence 53, Appl |
| c 517 | 19 | 1.3 | 493 | 12 | US-10-007-805-53 | Sequence 53, Appl |
| c 518 | 19 | 1.3 | 494 | 10 | US-09-920-300A-70 | Sequence 70, Appl |
| c 519 | 19 | 1.3 | 494 | 12 | US-10-033-528-70 | Sequence 70, Appl |
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| c 521 | 19 | 1.3 | 499 | 9 | US-09-232-880-73 | Sequence 73, Appl |
| c 522 | 19 | 1.3 | 499 | 9 | US-10-012-896-73 | Sequence 73, Appl |
| c 523 | 19 | 1.3 | 499 | 9 | US-09-895-793-73 | Sequence 73, Appl |
| c 524 | 19 | 1.3 | 499 | 9 | US-09-895-814-73 | Sequence 73, Appl |
| c 525 | 19 | 1.3 | 499 | 10 | US-09-759-143-73 | Sequence 73, Appl |
| c 526 | 19 | 1.3 | 499 | 10 | US-09-780-669-73 | Sequence 73, Appl |
| c 527 | 19 | 1.3 | 499 | 10 | US-09-030-606-73 | Sequence 73, Appl |
| c 528 | 19 | 1.3 | 499 | 10 | US-09-822-827-73 | Sequence 73, Appl |
| c 529 | 19 | 1.3 | 499 | 10 | US-09-115-453-73 | Sequence 73, Appl |
| c 530 | 19 | 1.3 | 502 | 9 | US-10-202-193-194 | Sequence 194, App |

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| | 532 | 19 | 1.3 | 514 | 9 | US-09-736-457-1656 Sequence 1656, Ap |
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| | 534 | 19 | 1.3 | 514 | 9 | US-09-849-626-1656 Sequence 1656, Ap |
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| | 538 | 19 | 1.3 | 546 | 10 | US-09-735-705-129 Sequence 129, App |
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| | 540 | 19 | 1.3 | 546 | 10 | US-09-897-778-129 Sequence 129, App |
| c | 541 | 19 | 1.3 | 553 | 9 | US-10-076-622-152 Sequence 152, App |
| c | 542 | 19 | 1.3 | 553 | 10 | US-09-789-561-37 Sequence 37, Appl |
| c | 543 | 19 | 1.3 | 553 | 10 | US-09-604-287A-152 Sequence 152, App |
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| c | 545 | 19 | 1.3 | 553 | 12 | US-10-007-805-152 Sequence 152, App |
| c | 546 | 19 | 1.3 | 561 | 9 | US-09-796-692-4222 Sequence 4222, Ap |
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| c | 549 | 19 | 1.3 | 577 | 10 | US-09-815-343-119 Sequence 119, App |
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| c | 551 | 19 | 1.3 | 578 | 10 | US-09-604-287A-150 Sequence 150, App |
| c | 552 | 19 | 1.3 | 578 | 10 | US-09-339-338-150 Sequence 150, App |
| c | 553 | 19 | 1.3 | 578 | 12 | US-10-007-805-150 Sequence 150, App |
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| | 560 | 19 | 1.3 | 605 | 9 | US-09-736-457-1657 Sequence 1657, Ap |
| | 561 | 19 | 1.3 | 605 | 9 | US-09-902-941-1657 Sequence 1657, Ap |
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| | 565 | 19 | 1.3 | 643 | 10 | US-09-815-343-408 Sequence 408, App |
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| | 586 | 19 | 1.3 | 724 | 9 | US-10-202-193-311 Sequence 311, App |
| | 587 | 19 | 1.3 | 724 | 9 | US-10-202-193-327 Sequence 327, App |
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| | 592 | 19 | 1.3 | 726 | 9 | US-10-202-193-287 Sequence 287, App |
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| | 594 | 19 | 1.3 | 727 | 9 | US-10-202-193-279 Sequence 279, App |
| | 595 | 19 | 1.3 | 727 | 9 | US-10-202-193-281 Sequence 281, App |
| | 596 | 19 | 1.3 | 727 | 9 | US-10-202-193-331 Sequence 331, App |
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| | 598 | 19 | 1.3 | 729 | 10 | US-09-827-669-58 Sequence 58, Appl |
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| | 607 | 19 | 1.3 | 736 | 9 | US-10-202-193-272 Sequence 272, App |
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| | 612 | 19 | 1.3 | 739 | 10 | US-09-826-508-7 Sequence 7, Appli |
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| | 615 | 19 | 1.3 | 740 | 9 | US-10-202-193-314 Sequence 314, App |
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| | 623 | 19 | 1.3 | 744 | 9 | US-10-202-193-276 Sequence 276, App |
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| | 629 | 19 | 1.3 | 745 | 9 | US-10-202-193-302 Sequence 302, App |
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| | 631 | 19 | 1.3 | 746 | 9 | US-10-202-193-306 Sequence 306, App |
| | 632 | 19 | 1.3 | 746 | 9 | US-10-202-193-309 Sequence 309, App |
| | 633 | 19 | 1.3 | 746 | 9 | US-10-202-193-324 Sequence 324, App |
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| | 635 | 19 | 1.3 | 747 | 9 | US-10-202-193-326 Sequence 326, App |
| | 636 | 19 | 1.3 | 747 | 9 | US-10-202-193-328 Sequence 328, App |
| | 637 | 19 | 1.3 | 748 | 9 | US-10-202-193-278 Sequence 278, App |
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| | 639 | 19 | 1.3 | 751 | 9 | US-10-202-193-310 Sequence 310, App |
| | 640 | 19 | 1.3 | 752 | 9 | US-10-202-193-264 Sequence 264, App |
| | 641 | 19 | 1.3 | 757 | 9 | US-10-202-193-286 Sequence 286, App |
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| | 648 | 19 | 1.3 | 771 | 9 | US-10-202-193-150 Sequence 150, App |
| | 649 | 19 | 1.3 | 771 | 9 | US-10-202-193-160 Sequence 160, App |
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| | 654 | 19 | 1.3 | 772 | 9 | US-10-202-193-173 Sequence 173, App |
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| | 656 | 19 | 1.3 | 773 | 9 | US-10-202-193-164 Sequence 164, App |
| | 657 | 19 | 1.3 | 773 | 9 | US-10-202-193-176 Sequence 176, App |
| | 658 | 19 | 1.3 | 774 | 9 | US-10-202-193-129 Sequence 129, App |
| | 659 | 19 | 1.3 | 775 | 9 | US-10-202-193-133 Sequence 133, App |
| | 660 | 19 | 1.3 | 775 | 9 | US-10-202-193-148 Sequence 148, App |
| | 661 | 19 | 1.3 | 775 | 9 | US-10-202-193-166 Sequence 166, App |
| | 662 | 19 | 1.3 | 777 | 9 | US-10-202-193-137 Sequence 137, App |
| | 663 | 19 | 1.3 | 778 | 9 | US-10-202-193-146 Sequence 146, App |
| | 664 | 19 | 1.3 | 779 | 9 | US-10-202-193-139 Sequence 139, App |
| | 665 | 19 | 1.3 | 779 | 9 | US-10-202-193-140 Sequence 140, App |
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| | 667 | 19 | 1.3 | 780 | 9 | US-10-202-193-142 Sequence 142, App |
| c | 668 | 19 | 1.3 | 780 | 9 | US-10-202-193-168 Sequence 168, App |
| | 669 | 19 | 1.3 | 782 | 9 | US-10-202-193-144 Sequence 144, App |
| | 670 | 19 | 1.3 | 782 | 9 | US-10-202-193-171 Sequence 171, App |
| | 671 | 19 | 1.3 | 784 | 9 | US-10-202-193-135 Sequence 135, App |
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| | 683 | 19 | 1.3 | 813 | 9 | US-10-202-193-114 | Sequence 114, App |
| | 684 | 19 | 1.3 | 814 | 9 | US-10-202-193-257 | Sequence 257, App |
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| | 689 | 19 | 1.3 | 815 | 9 | US-10-202-193-229 | Sequence 229, App |
| | 690 | 19 | 1.3 | 815 | 9 | US-10-202-193-238 | Sequence 238, App |
| | 691 | 19 | 1.3 | 815 | 9 | US-10-202-193-240 | Sequence 240, App |
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| | 693 | 19 | 1.3 | 816 | 9 | US-10-202-193-247 | Sequence 247, App |
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| | 696 | 19 | 1.3 | 818 | 9 | US-10-202-193-116 | Sequence 116, App |
| | 697 | 19 | 1.3 | 818 | 9 | US-10-202-193-131 | Sequence 131, App |
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| | 699 | 19 | 1.3 | 819 | 9 | US-10-202-193-203 | Sequence 203, App |
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| | 701 | 19 | 1.3 | 820 | 9 | US-10-202-193-206 | Sequence 206, App |
| | 702 | 19 | 1.3 | 820 | 9 | US-10-202-193-210 | Sequence 210, App |
| | 703 | 19 | 1.3 | 821 | 9 | US-10-202-193-212 | Sequence 212, App |
| | 704 | 19 | 1.3 | 821 | 9 | US-10-202-193-249 | Sequence 249, App |
| | 705 | 19 | 1.3 | 822 | 9 | US-10-202-193-187 | Sequence 187, App |
| | 706 | 19 | 1.3 | 822 | 9 | US-10-202-193-223 | Sequence 223, App |
| | 707 | 19 | 1.3 | 822 | 9 | US-10-202-193-225 | Sequence 225, App |
| | 708 | 19 | 1.3 | 822 | 9 | US-10-202-193-245 | Sequence 245, App |
| | 709 | 19 | 1.3 | 823 | 9 | US-10-202-193-180 | Sequence 180, App |
| | 710 | 19 | 1.3 | 823 | 9 | US-10-202-193-216 | Sequence 216, App |
| | 711 | 19 | 1.3 | 824 | 9 | US-10-202-193-184 | Sequence 184, App |
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| | 714 | 19 | 1.3 | 827 | 9 | US-10-202-193-156 | Sequence 156, App |
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| | 717 | 19 | 1.3 | 830 | 9 | US-10-202-193-182 | Sequence 182, App |
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| | 720 | 19 | 1.3 | 831 | 9 | US-10-202-193-221 | Sequence 221, App |
| | 721 | 19 | 1.3 | 831 | 9 | US-10-202-193-253 | Sequence 253, App |
| | 722 | 19 | 1.3 | 833 | 9 | US-10-202-193-125 | Sequence 125, App |
| | 723 | 19 | 1.3 | 834 | 9 | US-10-202-193-193 | Sequence 193, App |
| | 724 | 19 | 1.3 | 837 | 9 | US-10-202-193-199 | Sequence 199, App |
| | 725 | 19 | 1.3 | 840 | 9 | US-10-202-193-204 | Sequence 204, App |
| | 726 | 19 | 1.3 | 842 | 9 | US-10-202-193-189 | Sequence 189, App |
| | 727 | 19 | 1.3 | 848 | 9 | US-10-202-193-195 | Sequence 195, App |
| | 728 | 19 | 1.3 | 864 | 9 | US-10-202-193-123 | Sequence 123, App |
| c | 729 | 19 | 1.3 | 870 | 10 | US-09-371-307-3 | Sequence 3, Appli |
| c | 730 | 19 | 1.3 | 885 | 9 | US-09-768-020-49 | Sequence 49, Appl |
| c | 731 | 19 | 1.3 | 918 | 9 | US-09-986-480-159 | Sequence 159, App |
| c | 732 | 19 | 1.3 | 950 | 9 | US-10-202-193-138 | Sequence 138, App |
| | 733 | 19 | 1.3 | 960 | 12 | US-10-041-472-2 | Sequence 2, Appli |
| c | 734 | 19 | 1.3 | 977 | 9 | US-09-768-020-53 | Sequence 53, Appl |
| c | 735 | 19 | 1.3 | 999 | 9 | US-10-125-470-8 | Sequence 8, Appli |
| | 736 | 19 | 1.3 | 999 | 9 | US-09-736-457-1664 | Sequence 1664, Ap |
| | 737 | 19 | 1.3 | 999 | 9 | US-09-902-941-1664 | Sequence 1664, Ap |
| c | 738 | 19 | 1.3 | 999 | 9 | US-10-125-452-8 | Sequence 8, Appli |
| c | 739 | 19 | 1.3 | 999 | 9 | US-09-955-504-8 | Sequence 8, Appli |
| | 740 | 19 | 1.3 | 999 | 9 | US-09-849-626-1664 | Sequence 1664, Ap |
| c | 741 | 19 | 1.3 | 999 | 9 | US-09-986-480-69 | Sequence 69, Appl |
| | 742 | 19 | 1.3 | 1008 | 9 | US-10-202-193-16 | Sequence 16, Appl |
| c | 743 | 19 | 1.3 | 1009 | 10 | US-09-804-682-35 | Sequence 35, Appl |
| c | 744 | 19 | 1.3 | 1012 | 10 | US-09-398-399-20 | Sequence 20, Appl |
| c | 745 | 19 | 1.3 | 1012 | 10 | US-09-899-381-20 | Sequence 20, Appl |
| | 746 | 19 | 1.3 | 1013 | 9 | US-10-202-193-14 | Sequence 14, Appl |
| | 747 | 19 | 1.3 | 1017 | 9 | US-10-202-193-48 | Sequence 48, Appl |
| | 748 | 19 | 1.3 | 1019 | 9 | US-10-202-193-31 | Sequence 31, Appl |
| | 749 | 19 | 1.3 | 1020 | 9 | US-10-202-193-13 | Sequence 13, Appl |
| | 750 | 19 | 1.3 | 1020 | 9 | US-10-202-193-42 | Sequence 42, Appl |
| c | 751 | 19 | 1.3 | 1020 | 9 | US-10-202-193-102 | Sequence 102, App |
| | 752 | 19 | 1.3 | 1021 | 9 | US-10-202-193-103 | Sequence 103, App |
| c | 753 | 19 | 1.3 | 1023 | 10 | US-09-804-682-24 | Sequence 24, Appl |
| c | 754 | 19 | 1.3 | 1024 | 9 | US-10-202-193-9 | Sequence 9, Appli |
| | 755 | 19 | 1.3 | 1024 | 9 | US-10-202-193-11 | Sequence 11, Appl |
| | 756 | 19 | 1.3 | 1024 | 9 | US-10-202-193-17 | Sequence 17, Appl |
| | 757 | 19 | 1.3 | 1024 | 9 | US-10-202-193-22 | Sequence 22, Appl |
| | 758 | 19 | 1.3 | 1024 | 9 | US-10-202-193-26 | Sequence 26, Appl |
| | 759 | 19 | 1.3 | 1024 | 9 | US-10-202-193-30 | Sequence 30, Appl |
| | 760 | 19 | 1.3 | 1024 | 9 | US-10-202-193-44 | Sequence 44, Appl |
| c | 761 | 19 | 1.3 | 1024 | 9 | US-10-202-193-45 | Sequence 45, Appl |
| | 762 | 19 | 1.3 | 1024 | 9 | US-10-202-193-46 | Sequence 46, Appl |
| c | 763 | 19 | 1.3 | 1024 | 9 | US-10-202-193-47 | Sequence 47, Appl |
| | 764 | 19 | 1.3 | 1024 | 9 | US-10-202-193-50 | Sequence 50, Appl |
| | 765 | 19 | 1.3 | 1024 | 9 | US-10-202-193-52 | Sequence 52, Appl |
| | 766 | 19 | 1.3 | 1024 | 9 | US-10-202-193-54 | Sequence 54, Appl |
| | 767 | 19 | 1.3 | 1024 | 9 | US-10-202-193-56 | Sequence 56, Appl |
| | 768 | 19 | 1.3 | 1024 | 9 | US-10-202-193-58 | Sequence 58, Appl |
| c | 769 | 19 | 1.3 | 1024 | 9 | US-10-202-193-59 | Sequence 59, Appl |
| | 770 | 19 | 1.3 | 1024 | 9 | US-10-202-193-60 | Sequence 60, Appl |
| c | 771 | 19 | 1.3 | 1024 | 9 | US-10-202-193-61 | Sequence 61, Appl |
| | 772 | 19 | 1.3 | 1024 | 9 | US-10-202-193-62 | Sequence 62, Appl |
| | 773 | 19 | 1.3 | 1024 | 9 | US-10-202-193-64 | Sequence 64, Appl |
| | 774 | 19 | 1.3 | 1024 | 9 | US-10-202-193-66 | Sequence 66, Appl |
| | 775 | 19 | 1.3 | 1024 | 9 | US-10-202-193-68 | Sequence 68, Appl |
| c | 776 | 19 | 1.3 | 1024 | 9 | US-10-202-193-69 | Sequence 69, Appl |
| | 777 | 19 | 1.3 | 1024 | 9 | US-10-202-193-70 | Sequence 70, Appl |
| | 778 | 19 | 1.3 | 1024 | 9 | US-10-202-193-72 | Sequence 72, Appl |
| | 779 | 19 | 1.3 | 1024 | 9 | US-10-202-193-74 | Sequence 74, Appl |
| | 780 | 19 | 1.3 | 1024 | 9 | US-10-202-193-76 | Sequence 76, Appl |
| c | 781 | 19 | 1.3 | 1024 | 9 | US-10-202-193-77 | Sequence 77, Appl |
| | 782 | 19 | 1.3 | 1024 | 9 | US-10-202-193-78 | Sequence 78, Appl |
| c | 783 | 19 | 1.3 | 1024 | 9 | US-10-202-193-79 | Sequence 79, Appl |
| | 784 | 19 | 1.3 | 1024 | 9 | US-10-202-193-80 | Sequence 80, Appl |
| | 785 | 19 | 1.3 | 1024 | 9 | US-10-202-193-82 | Sequence 82, Appl |
| | 786 | 19 | 1.3 | 1024 | 9 | US-10-202-193-84 | Sequence 84, Appl |
| | 787 | 19 | 1.3 | 1024 | 9 | US-10-202-193-86 | Sequence 86, Appl |
| c | 788 | 19 | 1.3 | 1024 | 9 | US-10-202-193-87 | Sequence 87, Appl |
| | 789 | 19 | 1.3 | 1024 | 9 | US-10-202-193-88 | Sequence 88, Appl |
| | 790 | 19 | 1.3 | 1024 | 9 | US-10-202-193-90 | Sequence 90, Appl |
| | 791 | 19 | 1.3 | 1024 | 9 | US-10-202-193-94 | Sequence 94, Appl |
| | 792 | 19 | 1.3 | 1024 | 9 | US-10-202-193-96 | Sequence 96, Appl |
| c | 793 | 19 | 1.3 | 1024 | 9 | US-10-202-193-97 | Sequence 97, Appl |
| | 794 | 19 | 1.3 | 1024 | 9 | US-10-202-193-98 | Sequence 98, Appl |
| c | 795 | 19 | 1.3 | 1024 | 9 | US-10-202-193-99 | Sequence 99, Appl |
| | 796 | 19 | 1.3 | 1024 | 9 | US-10-202-193-100 | Sequence 100, App |
| | 797 | 19 | 1.3 | 1024 | 9 | US-10-202-193-105 | Sequence 105, App |
| | 798 | 19 | 1.3 | 1024 | 9 | US-10-202-193-107 | Sequence 107, App |
| c | 799 | 19 | 1.3 | 1033 | 10 | US-09-804-682-23 | Sequence 23, Appl |
| | 800 | 19 | 1.3 | 1034 | 9 | US-09-736-457-1654 | Sequence 1654, Ap |
| | 801 | 19 | 1.3 | 1034 | 9 | US-09-902-941-1654 | Sequence 1654, Ap |
| | 802 | 19 | 1.3 | 1034 | 9 | US-09-849-626-1654 | Sequence 1654, Ap |
| | 803 | 19 | 1.3 | 1063 | 10 | US-09-804-682-18 | Sequence 18, Appl |
| c | 804 | 19 | 1.3 | 1085 | 10 | US-09-854-122-41 | Sequence 41, Appl |
| c | 805 | 19 | 1.3 | 1155 | 10 | US-09-804-682-5 | Sequence 5, Appli |
| | 806 | 19 | 1.3 | 1167 | 9 | US-10-098-841-327 | Sequence 327, App |
| | 807 | 19 | 1.3 | 1170 | 10 | US-09-804-682-10 | Sequence 10, Appl |
| | 808 | 19 | 1.3 | 1175 | 10 | US-09-850-351A-143 | Sequence 143, App |
| c | 809 | 19 | 1.3 | 1204 | 10 | US-09-398-399-21 | Sequence 21, Appl |
| c | 810 | 19 | 1.3 | 1204 | 10 | US-09-899-381-21 | Sequence 21, Appl |
| | 811 | 19 | 1.3 | 1259 | 10 | US-09-809-545A-40 | Sequence 40, Appl |
| | 812 | 19 | 1.3 | 1263 | 9 | US-09-938-842A-919 | Sequence 919, App |
| | 813 | 19 | 1.3 | 1272 | 12 | US-10-041-472-3 | Sequence 3, Appli |
| c | 814 | 19 | 1.3 | 1392 | 10 | US-09-398-399-23 | Sequence 23, Appl |
| c | 815 | 19 | 1.3 | 1392 | 10 | US-09-899-381-23 | Sequence 23, Appl |
| c | 816 | 19 | 1.3 | 1394 | 10 | US-09-398-399-22 | Sequence 22, Appl |
| c | 817 | 19 | 1.3 | 1394 | 10 | US-09-899-381-22 | Sequence 22, Appl |
| | 818 | 19 | 1.3 | 1411 | 10 | US-09-837-751-3 | Sequence 3, Appli |
| c | 819 | 19 | 1.3 | 1436 | 10 | US-09-788-345-11 | Sequence 11, Appl |
| | 820 | 19 | 1.3 | 1454 | 9 | US-10-096-571-7 | Sequence 7, Appli |
| c | 821 | 19 | 1.3 | 1464 | 10 | US-09-841-132-348 | Sequence 348, App |
| | 822 | 19 | 1.3 | 1486 | 10 | US-09-967-552A-17 | Sequence 17, Appl |

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| c 823 | 19 | 1.3 | 1557 | 10 | US-09-841-132-332 | Sequence 332, App |
| 824 | 19 | 1.3 | 1668 | 10 | US-09-750-373-12 | Sequence 12, Appl |
| 825 | 19 | 1.3 | 1740 | 9 | US-09-938-842A-2315 | Sequence 2315, Ap |
| 826 | 19 | 1.3 | 1741 | 10 | US-09-855-544A-5 | Sequence 5, Appli |
| c 827 | 19 | 1.3 | 1752 | 10 | US-09-841-132-352 | Sequence 352, App |
| c 828 | 19 | 1.3 | 1758 | 10 | US-09-841-132-336 | Sequence 336, App |
| 829 | 19 | 1.3 | 1839 | 10 | US-09-938-970-3 | Sequence 3, Appli |
| c 830 | 19 | 1.3 | 1860 | 10 | US-09-841-132-308 | Sequence 308, App |
| c 831 | 19 | 1.3 | 1896 | 10 | US-09-841-132-324 | Sequence 324, App |
| c 832 | 19 | 1.3 | 1902 | 9 | US-09-938-842A-1750 | Sequence 1750, Ap |
| c 833 | 19 | 1.3 | 1941 | 10 | US-09-841-132-316 | Sequence 316, App |
| c 834 | 19 | 1.3 | 1965 | 10 | US-09-841-132-340 | Sequence 340, App |
| c 835 | 19 | 1.3 | 2010 | 9 | US-10-024-632-8 | Sequence 8, Appli |
| c 836 | 19 | 1.3 | 2049 | 10 | US-09-887-576-267 | Sequence 267, App |
| c 837 | 19 | 1.3 | 2052 | 10 | US-09-841-132-356 | Sequence 356, App |
| c 838 | 19 | 1.3 | 2076 | 10 | US-09-841-132-312 | Sequence 312, App |
| 839 | 19 | 1.3 | 2082 | 9 | US-09-893-519A-105 | Sequence 105, App |
| c 840 | 19 | 1.3 | 2103 | 10 | US-09-841-132-344 | Sequence 344, App |
| c 841 | 19 | 1.3 | 2148 | 10 | US-09-841-132-320 | Sequence 320, App |
| c 842 | 19 | 1.3 | 2148 | 10 | US-09-841-132-328 | Sequence 328, App |
| 843 | 19 | 1.3 | 2184 | 9 | US-10-097-597-2 | Sequence 2, Appli |
| 844 | 19 | 1.3 | 2184 | 9 | US-10-097-580-2 | Sequence 2, Appli |
| 845 | 19 | 1.3 | 2184 | 10 | US-09-445-023A-2 | Sequence 2, Appli |
| 846 | 19 | 1.3 | 2259 | 10 | US-09-964-824A-577 | Sequence 577, App |
| 847 | 19 | 1.3 | 2259 | 10 | US-09-880-107-2107 | Sequence 2107, Ap |
| 848 | 19 | 1.3 | 2259 | 10 | US-09-967-768A-137 | Sequence 137, App |
| c 849 | 19 | 1.3 | 2267 | 9 | US-09-961-077-25 | Sequence 25, Appl |
| 850 | 19 | 1.3 | 2293 | 9 | US-10-098-841-3 | Sequence 3, Appli |
| 851 | 19 | 1.3 | 2345 | 10 | US-09-981-649A-29 | Sequence 29, Appl |
| 852 | 19 | 1.3 | 2360 | 10 | US-09-981-649A-27 | Sequence 27, Appl |
| 853 | 19 | 1.3 | 2389 | 10 | US-09-800-729-51 | Sequence 51, Appl |
| 854 | 19 | 1.3 | 2464 | 10 | US-09-800-729-214 | Sequence 214, App |
| c 855 | 19 | 1.3 | 2794 | 10 | US-09-917-800A-1663 | Sequence 1663, Ap |
| 856 | 19 | 1.3 | 2910 | 10 | US-09-989-002-10 | Sequence 10, Appl |
| 857 | 19 | 1.3 | 2919 | 10 | US-09-765-344-1 | Sequence 1, Appli |
| 858 | 19 | 1.3 | 2932 | 10 | US-09-938-970-1 | Sequence 1, Appli |
| 859 | 19 | 1.3 | 2955 | 9 | US-09-772-180A-3 | Sequence 3, Appli |
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| 862 | 19 | 1.3 | 3064 | 9 | US-10-012-896-774 | Sequence 774, App |
| 863 | 19 | 1.3 | 3064 | 9 | US-09-895-793-774 | Sequence 774, App |
| 864 | 19 | 1.3 | 3064 | 9 | US-09-895-814-774 | Sequence 774, App |
| 865 | 19 | 1.3 | 3064 | 10 | US-09-756-976-1 | Sequence 1, Appli |
| 866 | 19 | 1.3 | 3064 | 10 | US-09-759-143-774 | Sequence 774, App |
| 867 | 19 | 1.3 | 3064 | 10 | US-09-780-669-774 | Sequence 774, App |
| 868 | 19 | 1.3 | 3064 | 10 | US-09-822-827-774 | Sequence 774, App |
| 869 | 19 | 1.3 | 3540 | 10 | US-09-962-805-5 | Sequence 5, Appli |
| c 870 | 19 | 1.3 | 3639 | 9 | US-10-012-896-779 | Sequence 779, App |
| c 871 | 19 | 1.3 | 3639 | 9 | US-09-895-793-779 | Sequence 779, App |
| c 872 | 19 | 1.3 | 3639 | 9 | US-09-895-814-779 | Sequence 779, App |
| c 873 | 19 | 1.3 | 3639 | 10 | US-09-759-143-779 | Sequence 779, App |
| c 874 | 19 | 1.3 | 3639 | 10 | US-09-780-669-779 | Sequence 779, App |
| c 875 | 19 | 1.3 | 3639 | 10 | US-09-822-827-779 | Sequence 779, App |
| 876 | 19 | 1.3 | 3900 | 10 | US-09-764-864-1705 | Sequence 1705, Ap |
| c 877 | 19 | 1.3 | 3901 | 10 | US-09-764-864-1703 | Sequence 1703, Ap |
| c 878 | 19 | 1.3 | 3906 | 9 | US-09-935-280-17 | Sequence 17, Appl |
| c 879 | 19 | 1.3 | 4400 | 10 | US-09-853-386-47 | Sequence 47, Appl |
| c 880 | 19 | 1.3 | 4400 | 12 | US-10-005-169-3 | Sequence 3, Appli |
| c 881 | 19 | 1.3 | 4613 | 9 | US-10-001-189-46 | Sequence 46, Appl |
| c 882 | 19 | 1.3 | 5285 | 9 | US-10-038-001-1 | Sequence 1, Appli |
| c 883 | 19 | 1.3 | 5856 | 10 | US-09-836-077-34 | Sequence 34, Appl |
| c 884 | 19 | 1.3 | 6148 | 9 | US-09-884-211A-5 | Sequence 5, Appli |
| c 885 | 19 | 1.3 | 6149 | 9 | US-09-884-211A-6 | Sequence 6, Appli |
| c 886 | 19 | 1.3 | 6186 | 10 | US-09-780-933-5 | Sequence 5, Appli |
| c 887 | 19 | 1.3 | 6200 | 9 | US-09-993-241-1 | Sequence 1, Appli |
| c 888 | 19 | 1.3 | 6200 | 9 | US-10-206-443-1 | Sequence 1, Appli |
| c 889 | 19 | 1.3 | 6200 | 10 | US-09-993-038-1 | Sequence 1, Appli |
| c 890 | 19 | 1.3 | 6213 | 10 | US-09-780-933-7 | Sequence 7, Appli |
| c 891 | 19 | 1.3 | 7367 | 9 | US-10-024-632-7 | Sequence 7, Appli |
| c 892 | 19 | 1.3 | 9668 | 10 | US-09-801-574-54 | Sequence 54, Appl |
| c 893 | 19 | 1.3 | 10062 | 10 | US-09-888-615-5 | Sequence 5, Appli |
| 894 | 19 | 1.3 | 31766 | 10 | US-09-765-344-5 | Sequence 5, Appli |
| 895 | 19 | 1.3 | 659158 | 9 | US-09-771-208-20 | Sequence 20, Appl |
| c 896 | 19 | 1.3 | 684973 | 10 | US-09-263-959-1 | Sequence 1, Appli |
| c 897 | 18 | 1.2 | 18 | 10 | US-09-263-959-921 | Sequence 921, App |
| c 898 | 18 | 1.2 | 25 | 10 | US-09-814-986-59 | Sequence 59, Appl |
| 899 | 18 | 1.2 | 26 | 9 | US-09-811-824-5 | Sequence 5, Appli |
| c 900 | 18 | 1.2 | 28 | 9 | US-09-925-664-25 | Sequence 25, Appl |
| 901 | 18 | 1.2 | 30 | 10 | US-09-045-620-3 | Sequence 3, Appli |
| 902 | 18 | 1.2 | 30 | 10 | US-09-954-697-50 | Sequence 50, Appl |
| c 903 | 18 | 1.2 | 34 | 9 | US-09-811-824-4 | Sequence 4, Appli |
| 904 | 18 | 1.2 | 42 | 10 | US-09-888-358-7 | Sequence 7, Appli |
| c 905 | 18 | 1.2 | 46 | 9 | US-09-996-634-108 | Sequence 108, App |
| 906 | 18 | 1.2 | 46 | 9 | US-10-026-914-8 | Sequence 8, Appli |
| 907 | 18 | 1.2 | 46 | 9 | US-10-026-914-10 | Sequence 10, Appl |
| 908 | 18 | 1.2 | 46 | 9 | US-10-026-914-14 | Sequence 14, Appl |
| 909 | 18 | 1.2 | 46 | 9 | US-10-026-914-16 | Sequence 16, Appl |
| 910 | 18 | 1.2 | 47 | 9 | US-10-026-914-4 | Sequence 4, Appli |
| 911 | 18 | 1.2 | 48 | 10 | US-09-801-042-8 | Sequence 8, Appli |
| 912 | 18 | 1.2 | 48 | 12 | US-10-082-018-6 | Sequence 6, Appli |
| 913 | 18 | 1.2 | 50 | 10 | US-09-935-727-26 | Sequence 26, Appl |
| 914 | 18 | 1.2 | 51 | 9 | US-09-768-827-86 | Sequence 86, Appl |
| 915 | 18 | 1.2 | 52 | 10 | US-09-374-671-59 | Sequence 59, Appl |
| 916 | 18 | 1.2 | 56 | 10 | US-09-004-068-4 | Sequence 4, Appli |
| c 917 | 18 | 1.2 | 57 | 9 | US-10-210-296-80 | Sequence 80, Appl |
| 918 | 18 | 1.2 | 58 | 10 | US-09-777-430A-13 | Sequence 13, Appl |
| 919 | 18 | 1.2 | 62 | 9 | US-09-942-087A-34 | Sequence 34, Appl |
| c 920 | 18 | 1.2 | 62 | 9 | US-10-210-296-70 | Sequence 70, Appl |
| 921 | 18 | 1.2 | 62 | 10 | US-09-779-233-22 | Sequence 22, Appl |
| 922 | 18 | 1.2 | 69 | 9 | US-09-768-827-66 | Sequence 66, Appl |
| 923 | 18 | 1.2 | 71 | 9 | US-09-768-827-60 | Sequence 60, Appl |
| c 924 | 18 | 1.2 | 73 | 10 | US-09-037-657-34 | Sequence 34, Appl |
| 925 | 18 | 1.2 | 77 | 10 | US-09-844-508-39 | Sequence 39, Appl |
| c 926 | 18 | 1.2 | 83 | 10 | US-09-969-373-1234 | Sequence 1234, Ap |
| 927 | 18 | 1.2 | 96 | 10 | US-09-974-248-3 | Sequence 3, Appli |
| c 928 | 18 | 1.2 | 106 | 10 | US-09-900-530A-11 | Sequence 11, Appl |
| 929 | 18 | 1.2 | 115 | 10 | US-09-864-761-20283 | Sequence 20283, A |
| c 930 | 18 | 1.2 | 118 | 9 | US-09-942-087A-39 | Sequence 39, Appl |
| 931 | 18 | 1.2 | 118 | 9 | US-09-796-692-6689 | Sequence 6689, Ap |
| c 932 | 18 | 1.2 | 118 | 10 | US-09-779-233-26 | Sequence 26, Appl |
| c 933 | 18 | 1.2 | 126 | 10 | US-09-864-761-19220 | Sequence 19220, A |
| c 934 | 18 | 1.2 | 129 | 10 | US-09-867-701-4583 | Sequence 4583, Ap |
| c 935 | 18 | 1.2 | 147 | 10 | US-09-765-780A-17 | Sequence 17, Appl |
| c 936 | 18 | 1.2 | 147 | 10 | US-09-765-870-17 | Sequence 17, Appl |
| c 937 | 18 | 1.2 | 170 | 10 | US-09-765-780A-16 | Sequence 16, Appl |
| c 938 | 18 | 1.2 | 170 | 10 | US-09-765-870-16 | Sequence 16, Appl |
| c 939 | 18 | 1.2 | 187 | 9 | US-09-942-087A-37 | Sequence 37, Appl |
| c 940 | 18 | 1.2 | 187 | 10 | US-09-779-233-24 | Sequence 24, Appl |
| c 941 | 18 | 1.2 | 211 | 9 | US-09-954-531-296 | Sequence 296, App |
| c 942 | 18 | 1.2 | 214 | 9 | US-09-728-444-322 | Sequence 322, App |
| 943 | 18 | 1.2 | 234 | 10 | US-09-867-701-3715 | Sequence 3715, Ap |
| c 944 | 18 | 1.2 | 263 | 10 | US-09-004-068-2 | Sequence 2, Appli |
| c 945 | 18 | 1.2 | 269 | 10 | US-09-867-701-3630 | Sequence 3630, Ap |
| c 946 | 18 | 1.2 | 271 | 10 | US-09-867-701-5599 | Sequence 5599, Ap |
| 947 | 18 | 1.2 | 273 | 10 | US-09-878-574-5728 | Sequence 5728, Ap |
| c 948 | 18 | 1.2 | 277 | 9 | US-09-942-087A-38 | Sequence 38, Appl |
| c 949 | 18 | 1.2 | 277 | 10 | US-09-779-233-25 | Sequence 25, Appl |
| c 950 | 18 | 1.2 | 280 | 10 | US-09-004-068-5 | Sequence 5, Appli |
| c 951 | 18 | 1.2 | 280 | 10 | US-09-004-068-8 | Sequence 8, Appli |
| 952 | 18 | 1.2 | 286 | 10 | US-09-878-574-3064 | Sequence 3064, Ap |
| c 953 | 18 | 1.2 | 291 | 9 | US-10-012-896-823 | Sequence 823, App |
| c 954 | 18 | 1.2 | 291 | 9 | US-09-895-793-823 | Sequence 823, App |
| c 955 | 18 | 1.2 | 291 | 9 | US-09-895-814-823 | Sequence 823, App |
| c 956 | 18 | 1.2 | 291 | 10 | US-09-759-143-823 | Sequence 823, App |
| c 957 | 18 | 1.2 | 291 | 10 | US-09-780-669-823 | Sequence 823, App |
| c 958 | 18 | 1.2 | 291 | 10 | US-09-822-827-823 | Sequence 823, App |
| c 959 | 18 | 1.2 | 294 | 10 | US-09-334-477-22 | Sequence 22, Appl |
| c 960 | 18 | 1.2 | 294 | 10 | US-09-334-477-26 | Sequence 26, Appl |
| 961 | 18 | 1.2 | 300 | 9 | US-09-894-030-2 | Sequence 2, Appli |
| 962 | 18 | 1.2 | 300 | 10 | US-09-893-600-2 | Sequence 2, Appli |
| 963 | 18 | 1.2 | 300 | 10 | US-09-893-499-2 | Sequence 2, Appli |
| c 964 | 18 | 1.2 | 300 | 10 | US-09-867-701-4710 | Sequence 4710, Ap |
| c 965 | 18 | 1.2 | 301 | 9 | US-10-076-622-16 | Sequence 16, Appl |
| c 966 | 18 | 1.2 | 301 | 10 | US-09-604-287A-16 | Sequence 16, Appl |
| c 967 | 18 | 1.2 | 301 | 10 | US-09-339-338-16 | Sequence 16, Appl |
| c 968 | 18 | 1.2 | 301 | 12 | US-10-007-805-16 | Sequence 16, Appl |

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| c 969 | 18 | 1.2 | 312 | 10 | US-09-867-701-3198 | Sequence 3198, Ap |
| 970 | 18 | 1.2 | 360 | 9 | US-09-938-842A-324 | Sequence 324, App |
| c 971 | 18 | 1.2 | 402 | 10 | US-09-949-780-3 | Sequence 3, Appli |
| c 972 | 18 | 1.2 | 411 | 10 | US-09-960-352-12687 | Sequence 12687, A |
| c 973 | 18 | 1.2 | 412 | 10 | US-09-924-401-46 | Sequence 46, Appl |
| c 974 | 18 | 1.2 | 495 | 10 | US-09-798-789-1 | Sequence 1, Appli |
| 975 | 18 | 1.2 | 495 | 10 | US-09-864-761-3513 | Sequence 3513, Ap |
| c 976 | 18 | 1.2 | 495 | 10 | US-09-981-289-1 | Sequence 1, Appli |
| c 977 | 18 | 1.2 | 543 | 9 | US-09-876-348A-18 | Sequence 18, Appl |
| c 978 | 18 | 1.2 | 543 | 9 | US-09-876-348A-22 | Sequence 22, Appl |
| c 979 | 18 | 1.2 | 543 | 9 | US-09-876-348A-26 | Sequence 26, Appl |
| c 980 | 18 | 1.2 | 543 | 9 | US-09-876-348A-30 | Sequence 30, Appl |
| c 981 | 18 | 1.2 | 543 | 9 | US-09-876-348A-34 | Sequence 34, Appl |
| c 982 | 18 | 1.2 | 543 | 9 | US-09-876-348A-38 | Sequence 38, Appl |
| c 983 | 18 | 1.2 | 543 | 9 | US-09-876-796A-18 | Sequence 18, Appl |
| c 984 | 18 | 1.2 | 543 | 9 | US-09-876-796A-22 | Sequence 22, Appl |
| c 985 | 18 | 1.2 | 543 | 9 | US-09-876-796A-26 | Sequence 26, Appl |
| c 986 | 18 | 1.2 | 543 | 9 | US-09-876-796A-30 | Sequence 30, Appl |
| c 987 | 18 | 1.2 | 543 | 9 | US-09-876-796A-34 | Sequence 34, Appl |
| c 988 | 18 | 1.2 | 543 | 9 | US-09-876-796A-38 | Sequence 38, Appl |
| c 989 | 18 | 1.2 | 600 | 10 | US-09-263-959-400 | Sequence 400, App |
| c 990 | 18 | 1.2 | 630 | 9 | US-09-929-945-4 | Sequence 4, Appli |
| c 991 | 18 | 1.2 | 630 | 9 | US-09-929-945-6 | Sequence 6, Appli |
| c 992 | 18 | 1.2 | 630 | 10 | US-09-929-918-4 | Sequence 4, Appli |
| c 993 | 18 | 1.2 | 630 | 10 | US-09-929-918-6 | Sequence 6, Appli |
| 994 | 18 | 1.2 | 633 | 10 | US-09-809-545A-17 | Sequence 17, Appl |
| c 995 | 18 | 1.2 | 637 | 9 | US-09-991-496-25 | Sequence 25, Appl |
| c 996 | 18 | 1.2 | 637 | 10 | US-09-874-923-25 | Sequence 25, Appl |
| c 997 | 18 | 1.2 | 646 | 10 | US-09-804-682-139 | Sequence 139, App |
| c 998 | 18 | 1.2 | 681 | 9 | US-09-876-348A-16 | Sequence 16, Appl |
| c 999 | 18 | 1.2 | 681 | 9 | US-09-876-348A-28 | Sequence 28, Appl |
| c1000 | 18 | 1.2 | 681 | 9 | US-09-876-348A-36 | Sequence 36, Appl |

ALIGNMENTS

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RESULT 1
US-09-954-456-539
; Sequence 539, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 539
;   LENGTH: 2102
;   TYPE: DNA
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;   ORGANISM: Homo sapiens
US-09-954-456-539

  Query Match             90.8%;  Score 1356;  DB 10;  Length 2102;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
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Db       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
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Db     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
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Db     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
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Qy     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
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Db     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
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Db     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
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Db     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
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Db     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
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Db     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
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Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

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Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
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Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
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Db   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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RESULT 2
US-09-765-231A-6
; Sequence 6, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
; APPLICANT: Searle/Monsanto
; APPLICANT: Phippard, Deborah
; APPLICANT: Vasanthakamur, Geetha
; APPLICANT: Dotson, Stanton
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
; TITLE OF INVENTION: vectors, and cells
; FILE REFERENCE: SO-3221 PR
; CURRENT APPLICATION NUMBER: US/09/765,231A
; CURRENT FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 6
; LENGTH: 2263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 1-2263
; LOCATION: unknown
; OTHER INFORMATION: unsure at all n locations
US-09-765-231A-6

Query Match 82.1%; Score 1226; DB 10; Length 2263;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy    148 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 207
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Db    161 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 220

Qy    208 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 267
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Db    221 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 280

Qy    268 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 327
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Db    281 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 340

Qy    328 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 387
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 400

Qy    388 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 447
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Db    401 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 460

Qy    448 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 507
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 520

Qy    508 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 567
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 580

Qy    568 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 627
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Db    581 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 640

Qy    628 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 687
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Db    641 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 700

Qy    688 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 747
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 760

Qy    748 GCAACCAT-CTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 806
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Db    761 GCAACCATGCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 820

Qy    807 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 866
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 880

Qy    867 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 926
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Db    881 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 940

Qy    927 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 986
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Db    941 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 1000

Qy    987 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1046
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Db   1001 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1060

Qy   1047 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1106
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Db   1061 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1120

Qy   1107 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1166
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Db   1121 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1180

Qy   1167 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1226
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Db   1181 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1240

Qy   1227 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1286
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Db   1241 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1300

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Db   1301 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1360

Qy   1347 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1406
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Db   1361 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1420

Qy   1407 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1466
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Db   1421 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1480

Qy   1467 CTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db   1481 CTTTAAGATGTGTTAGGAATGTCAACA 1507


RESULT 3
US-09-964-824A-446/c
; Sequence 446, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
;  APPLICANT: Horrigan, Stephen
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-73
;  CURRENT APPLICATION NUMBER: US/09/964,824A
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: US/60/236,033
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,032
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,028
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 583
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 446
;   LENGTH: 586
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-824A-446

  Query Match             18.7%;  Score 279;  DB 10;  Length 586;
  Best Local Similarity   99.5%;  Pred. No. 2.1e-127;
  Matches  379;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1067 CCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCT 1126
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Db     426 CCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCT 367

Qy    1127 CACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGA 1186
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Db     366 CACCAACTTTTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGA 307

Qy    1187 GTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTG 1246
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Db     306 GTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTG 247

Qy    1247 GAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTT 1306
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Db     246 GAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTT 187

Qy    1307 TGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAA 1366
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Db     186 TGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAA 127

Qy    1367 ATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAA 1426
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Db     126 ATACACCCAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAA 67

Qy    1427 TAAATGCAATTGTGCTCTTCA 1447
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RESULT 4
US-09-867-701-9693
; Sequence 9693, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;  APPLICANT: Aglate, Paul A.
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE:  2001-05-29
;  NUMBER OF SEQ ID NOS: 10912
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9693
;   LENGTH: 368
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(368)
;   OTHER INFORMATION: n = A,T,C or G
US-09-867-701-9693

  Query Match             16.0%;  Score 239;  DB 10;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 1e-107;
  Matches  239;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 62

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      63 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 122

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     123 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 182

Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTG 376
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     183 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTG 241


RESULT 5
US-10-046-935-1922/c
; Sequence 1922, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.527C1
;  CURRENT APPLICATION NUMBER: US/10/046,935
;  CURRENT FILING DATE:  2002-01-15
;  NUMBER OF SEQ ID NOS: 2239
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1922
;   LENGTH: 221
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-046-935-1922

  Query Match             14.8%;  Score 221;  DB 9;  Length 221;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-99;
  Matches  221;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     779 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 838
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 162

Qy     839 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 898
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 102

Qy     899 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 958
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 42
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Qy    959 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 999
          ||||||||||||||||||||||||||||||||||||||||||
Db     41 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 1


RESULT 6
US-09-878-178-1922/c
; Sequence 1922, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.527
;  CURRENT APPLICATION NUMBER: US/09/878,178
;  CURRENT FILING DATE:  2001-06-08
;  NUMBER OF SEQ ID NOS: 2237
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1922
;   LENGTH: 221
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-878-178-1922

  Query Match             14.8%;  Score 221;  DB 9;  Length 221;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-99;
  Matches  221;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    779 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 162

Qy    839 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 102

Qy    899 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 958
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 42

Qy    959 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 999
          |||||||||||||||||||||||||||||||||||||||||
Db     41 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 1


RESULT 7
US-09-925-299-368
; Sequence 368, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 368
;   LENGTH: 548
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (370)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (378)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (384)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (412)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (429)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (449)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (471)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (490)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (495)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (528)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-368

  Query Match             13.1%;  Score 196;  DB 10;  Length 548;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-86;
  Matches  196;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    982 GAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCT 1041
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCT 68

Qy   1042 GAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACA 1101
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 GAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACA 128

Qy   1102 GTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACC 1161
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 GTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACC 188

Qy   1162 ACACCAAATGCTCAAG 1177
          ||||||||||||||||
Db    189 ACACCAAATGCTCAAG 204


RESULT 8
US-09-925-664-26
; Sequence 26, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 747
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
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;   NAME/KEY: CDS
;   LOCATION: (1)..(744)
;   OTHER INFORMATION:
US-09-925-664-26

  Query Match             7.7%;  Score 115;  DB 9;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 1e-46;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1230 CCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTG 1289
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 CCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTG 692

Qy   1290 TTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 TTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 747


RESULT 9
US-09-925-664-22
; Sequence 22, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 134
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-925-664-22

  Query Match             7.6%;  Score 114;  DB 9;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1231 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 69

Qy   1291 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 123


RESULT 10
US-09-925-664-23/c
; Sequence 23, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 134
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-925-664-23

  Query Match             7.6%;  Score 114;  DB 9;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1231 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 66

Qy   1291 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 12


RESULT 11
US-09-925-664-24
; Sequence 24, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 300
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-925-664-24

  Query Match             7.6%;  Score 114;  DB 9;  Length 300;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1231 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    100 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 159

Qy   1291 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    160 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 213


RESULT 12
US-09-925-664-29
; Sequence 29, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
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;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 786
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   NAME/KEY: CDS
;   LOCATION: (1)..(783)
;   OTHER INFORMATION:
US-09-925-664-29

  Query Match             7.6%;  Score 114;  DB 9;  Length 786;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-46;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1231 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    673 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 732

Qy   1291 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    733 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 786


RESULT 13
US-09-729-835-36
; Sequence 36, Application US/09729835
; Patent No. US20010016647A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 29 Human Secreted Proteins
;  FILE REFERENCE: PZ015P1
;  CURRENT APPLICATION NUMBER: US/09/729,835
;  CURRENT FILING DATE:  2000-12-06
;  PRIOR APPLICATION NUMBER: 09/257,179
;  PRIOR FILING DATE: 1999-02-25
;  PRIOR APPLICATION NUMBER: 60/056,270
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 60/056,271
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 60/056,247
;  PRIOR FILING DATE: 1997-08-29
;  PRIOR APPLICATION NUMBER: 60/056,073
;  PRIOR FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
;   LENGTH: 418
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (72)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (417)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-729-835-36

  Query Match             4.8%;  Score 71;  DB 10;  Length 418;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-25;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    776 GGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGT 835
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    287 GGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGT 346

Qy    836 GGAGTGACCCG 846
          ||||||||||||
Db    347 GGAGTGACCCG 357


RESULT 14
US-09-815-343-1286/c
; Sequence 1286, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
;  APPLICANT: Meagher, Madeleine
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  King, Gordon E.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.504
;  CURRENT APPLICATION NUMBER: US/09/815,343
;  CURRENT FILING DATE:  2001-03-22
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1286
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(479)
;   OTHER INFORMATION: n = A,T,C or G
US-09-815-343-1286

  Query Match             2.7%;  Score 40;  DB 10;  Length 479;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-10;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1454 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          ||||||||||||||||||||||||||||||||||||||||
Db    412 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 373


RESULT 15
US-09-847-101B-42/c
; Sequence 42, Application US/09847101B
; Publication No. US20020193327A1
; GENERAL INFORMATION:
;  APPLICANT: VON SEGGERN, DANIEL
;  APPLICANT:  NEMEROW, GLEN R.
;  APPLICANT:  FRIEDLANDER, MARTIN
;  TITLE OF INVENTION: VECTORS FOR OCULAR TRANSDUCTION AND USE THEREFOR FOR GENETIC T
;  FILE REFERENCE: 22908-1226B
;  CURRENT APPLICATION NUMBER: US/09/847,101B
;  CURRENT FILING DATE:  2001-05-01
;  PRIOR APPLICATION NUMBER: 09/562,934
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
;   LENGTH: 7231
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid pDV80
US-09-847-101B-42

  Query Match             2.2%;  Score 33;  DB 9;  Length 7231;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   33;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCT 33
          |||||||||||||||||||||||||||||||||
Db   3225 TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCT 3193
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Search completed: February 24, 2003, 09:25:07
Job time : 94.721 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 23, 2003, 20:11:42 ; Search time 315.627 Seconds
(without alignments)
10652.545 Million cell updates/sec

Title: US-09-623-035-5
Perfect score: 1493
Sequence: 1 tttaaacgggccctctagac.....atgtgttaggaatgtcaaca 1493

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1493 | 100.0 | 1493 | 20 | AAX87915 | Human tumour assoc |
| 2 | 1356 | 90.8 | 2015 | 8 | AAN70047 | Encodes human deca |
| 3 | 1356 | 90.8 | 2102 | 20 | AAX87914 | Human CD55 tumour |
| 4 | 1356 | 90.8 | 2102 | 24 | ABK83991 | Human cDNA differe |
| 5 | 1356 | 90.8 | 2102 | 24 | ABL65229 | Lung cancer relate |
| 6 | 1356 | 90.8 | 2115 | 10 | AAN91043 | Decay accelerating |
| 7 | 1356 | 90.8 | 2115 | 16 | AAQ79863 | Decay accelerating |
| 8 | 1356 | 90.8 | 2302 | 22 | AAH34999 | Human colon cancer |
| 9 | 1226 | 82.1 | 2263 | 22 | AAH23076 | Osteoarthritis tis |
| 10 | 1195 | 80.0 | 2096 | 16 | AAQ99105 | Human DAF cDNA. H |
| 11 | 1195 | 80.0 | 2096 | 18 | AAT84471 | Human DAF cDNA. H |
| 12 | 1146 | 76.8 | 1146 | 20 | AAV08935 | DAF protein coding |
| 13 | 1143 | 76.6 | 2233 | 8 | AAN70048 | Encodes human deca |
| 14 | 1143 | 76.6 | 2233 | 10 | AAN91044 | Membrane bound dec |
| 15 | 1143 | 76.6 | 2233 | 16 | AAQ79864 | Decay accelerating |
| 16 | 1097 | 73.5 | 2237 | 18 | AAT90287 | Human glycophospha |
| 17 | 1011 | 67.7 | 2416 | 22 | AAH57446 | Human lung cell sp |
| 18 | 970 | 65.0 | 1848 | 22 | AAD20355 | CAB2 protein encod |
| 19 | 970 | 65.0 | 1848 | 22 | AAD08170 | CAB-2 DNA. Uniden |
| 20 | 970 | 65.0 | 1848 | 24 | AAD27308 | CAB2 protein encod |
| 21 | 970 | 65.0 | 1878 | 17 | AAT46065 | Membrane co-factor |
| c 22 | 279 | 18.7 | 586 | 24 | ABL67412 | Thyroid cancer rel |
| 23 | 273 | 18.3 | 1925 | 22 | AAH72967 | Human cervical can |
| 24 | 239 | 16.0 | 368 | 24 | ABL86715 | Human ovarian canc |
| 25 | 231 | 15.5 | 1104 | 15 | AAQ58894 | Sequence encoding |
| c 26 | 221 | 14.8 | 224 | 24 | ABL38333 | Human colon tumour |
| 27 | 215 | 14.4 | 1077 | 20 | AAZ77541 | Human ovarian tumo |
| 28 | 196 | 13.1 | 548 | 21 | AAC98358 | Human colon cancer |
| 29 | 192 | 12.9 | 6565 | 22 | AAK91489 | Human digestive sy |
| 30 | 192 | 12.9 | 16141 | 22 | AAK73262 | Human immune/haema |
| 31 | 192 | 12.9 | 16141 | 22 | AAK91491 | Human digestive sy |
| 32 | 183 | 12.3 | 337 | 22 | AAL08160 | Human breast cance |
| 33 | 183 | 12.3 | 338 | 22 | AAL19070 | Human breast cance |
| 34 | 181 | 12.1 | 328 | 22 | AAL25905 | Human breast cance |
| 35 | 115 | 7.7 | 747 | 18 | AAT97175 | DR alpha-DAF chime |
| 36 | 114 | 7.6 | 134 | 18 | AAT97173 | Decay accelerating |
| 37 | 114 | 7.6 | 786 | 18 | AAT97176 | DR beta-1-DAF chim |
| 38 | 107 | 7.2 | 990 | 17 | AAT15927 | Neural cell adhesi |
| 39 | 71 | 4.8 | 418 | 20 | AAX30170 | Human secreted pro |
| c 40 | 70 | 4.7 | 227 | 21 | AAC18250 | Human secreted pro |
| c 41 | 61 | 4.1 | 61 | 22 | AAH57238 | Human lung specifi |
| 42 | 60 | 4.0 | 60 | 24 | ABN38712 | Human spliced tran |
| 43 | 52 | 3.5 | 3033 | 21 | AAZ29720 | Modified T. cruzi |
| c 44 | 44 | 2.9 | 44 | 16 | AAQ99120 | DAF oligo 176 -- 3 |
| c 45 | 40 | 2.7 | 479 | 23 | AAS58610 | cDNA #1286 encodin |
| 46 | 39 | 2.6 | 39 | 16 | AAQ99119 | DAF oligo 175 -- 5 |
| 47 | 34 | 2.3 | 35 | 22 | AAD20339 | PCR primer, DAFTH5 |
| 48 | 34 | 2.3 | 35 | 22 | AAD08154 | PCR primer CAB2H5- |
| 49 | 34 | 2.3 | 35 | 24 | AAD27292 | PCR primer, DAFTH5 |
| 50 | 34 | 2.3 | 39 | 24 | ABL52524 | Human DAF PCR prim |
| c 51 | 34 | 2.3 | 1241 | 24 | ABK87054 | DNA encoding mouse |
| c 52 | 34 | 2.3 | 1566 | 24 | ABK12874 | Chimeric SA-CD40L |
| c 53 | 34 | 2.3 | 4291 | 21 | AAA75084 | Complete nucleotid |
| c 54 | 33 | 2.2 | 1266 | 24 | ABK12871 | Chimeric TGF-B-SA |
| c 55 | 33 | 2.2 | 1329 | 24 | ABK12872 | Chimeric IL-2-SA D |
| c 56 | 33 | 2.2 | 1395 | 24 | ABK12873 | Chimeric IL-10-SA |
| c 57 | 33 | 2.2 | 1542 | 24 | ABK12870 | Chimeric B7.1-SA D |
| c 58 | 33 | 2.2 | 6050 | 22 | AAD10237 | Commercial plasmid |
| c 59 | 33 | 2.2 | 6567 | 22 | AAD06054 | Plasmid E2CLBDAS e |
| c 60 | 33 | 2.2 | 6623 | 22 | AAD06049 | Plasmid C7LBDAS en |
| c 61 | 33 | 2.2 | 6639 | 22 | AAD06055 | Plasmid E2CLBDBS e |
| c 62 | 33 | 2.2 | 6695 | 22 | AAD06051 | Plasmid C7LBDBS en |
| c 63 | 33 | 2.2 | 6695 | 22 | AAD06057 | Plasmid C7LBDBSG40 |
| c 64 | 33 | 2.2 | 6695 | 22 | AAD06058 | Plasmid C7LBDBSG52 |
| c 65 | 33 | 2.2 | 6746 | 22 | AAD06048 | Plasmid C7LBDAL en |
| c 66 | 33 | 2.2 | 6818 | 22 | AAD06050 | Plasmid C7LBDBL en |
| c 67 | 33 | 2.2 | 6828 | 22 | AAD06044 | Plasmid 2C7LBDAS e |
| c 68 | 33 | 2.2 | 6833 | 22 | AAD06053 | Plasmid C7LBDCS en |
| c 69 | 33 | 2.2 | 6900 | 22 | AAD06045 | Plasmid 2C7LBDBS e |
| c 70 | 33 | 2.2 | 6956 | 22 | AAD06052 | Plasmid C7LBDCL en |
| c 71 | 33 | 2.2 | 7038 | 22 | AAD06046 | Plasmid 2C7LBDCS e |
| c 72 | 33 | 2.2 | 7231 | 21 | AAA59090 | Nucleotide sequenc |
| c 73 | 33 | 2.2 | 7231 | 24 | ABA94286 | Nucleotide sequenc |
| 74 | 33 | 2.2 | 7475 | 20 | AAX02659 | EP-892047 Seq ID 3 |
| c 75 | 33 | 2.2 | 7586 | 24 | ABA92644 | Cholera toxin A1 s |
| c 76 | 33 | 2.2 | 7960 | 21 | AAA59072 | Nucleotide sequenc |
| c 77 | 33 | 2.2 | 7960 | 24 | ABA94274 | Nucleotide sequenc |
| c 78 | 33 | 2.2 | 7989 | 21 | AAA59075 | Nucleotide sequenc |
| c 79 | 33 | 2.2 | 7989 | 24 | ABA94277 | Nucleotide sequenc |
| 80 | 33 | 2.2 | 8192 | 20 | AAX02660 | EP-892047 Seq ID 3 |
| c 81 | 33 | 2.2 | 8578 | 21 | AAA07774 | DNA sequence of pl |
| c 82 | 32 | 2.1 | 72 | 24 | ABK55114 | Human colon cancer |

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 83 | 32 | 2.1 | 127 | 22 | AAC60394 | Construct pcDNA3-G |
| c | 84 | 32 | 2.1 | 396 | 22 | AAF94810 | Human ovarian canc |
| c | 85 | 32 | 2.1 | 396 | 24 | ABT03077 | Human ovarian carc |
| c | 86 | 32 | 2.1 | 396 | 24 | ABL48760 | Ovarian carcinoma |
| | 87 | 32 | 2.1 | 438 | 22 | AAH55685 | Human breast tumou |
| c | 88 | 32 | 2.1 | 482 | 23 | AAD23501 | Human lung tumour- |
| | 89 | 32 | 2.1 | 500 | 21 | AAZ99413 | Trans-spliced prod |
| | 90 | 32 | 2.1 | 500 | 24 | ABQ73502 | Pre-trans-splicing |
| c | 91 | 32 | 2.1 | 521 | 22 | AAS56432 | Human cDNA for an |
| | 92 | 32 | 2.1 | 707 | 22 | AAF95003 | Human ovarian canc |
| | 93 | 32 | 2.1 | 707 | 24 | ABT03270 | Human ovarian carc |
| | 94 | 32 | 2.1 | 707 | 24 | ABL48952 | Ovarian carcinoma |
| c | 95 | 32 | 2.1 | 998 | 24 | ABK55436 | Human colon cancer |
| c | 96 | 32 | 2.1 | 1247 | 24 | ABK12869 | Chimeric SA-FasL D |
| c | 97 | 32 | 2.1 | 1623 | 22 | AAD09263 | Delta VP22Cre-Stre |
| | 98 | 32 | 2.1 | 1637 | 20 | AAZ30973 | Porcine complement |
| c | 99 | 32 | 2.1 | 2001 | 20 | AAX99716 | Human Cterm mychis |
| c | 100 | 32 | 2.1 | 2001 | 22 | AAF24140 | C-terminal mychis |
| c | 101 | 32 | 2.1 | 2004 | 22 | AAD09259 | VP22-Cre fusion DN |
| c | 102 | 32 | 2.1 | 2010 | 20 | AAX99715 | Human C-term V5 hi |
| c | 103 | 32 | 2.1 | 2010 | 22 | AAF24139 | C-terminal V5 His |
| c | 104 | 32 | 2.1 | 2055 | 22 | AAD09268 | VP22CreStrepTag fu |
| c | 105 | 32 | 2.1 | 2247 | 22 | AAD09260 | VP22-Flpe fusion D |
| | 106 | 32 | 2.1 | 3373 | 24 | AAL39284 | Murine Toll-like r |
| c | 107 | 32 | 2.1 | 4488 | 22 | AAD09266 | pT7-VPCS vector DN |
| c | 108 | 32 | 2.1 | 5432 | 21 | AAZ89476 | Transgenic APP DNA |
| c | 109 | 32 | 2.1 | 5650 | 22 | AAH74866 | Nucleotide sequenc |
| c | 110 | 32 | 2.1 | 5695 | 24 | ABL58491 | Recombinant vector |
| c | 111 | 32 | 2.1 | 5695 | 24 | ABL58492 | Recombinant vector |
| c | 112 | 32 | 2.1 | 5731 | 22 | AAD11615 | Six finger ZFP (2C |
| c | 113 | 32 | 2.1 | 5953 | 22 | AAD09264 | pCRT7-delta VPCS v |
| c | 114 | 32 | 2.1 | 6082 | 22 | AAS63921 | Human prostate cDN |
| c | 115 | 32 | 2.1 | 6082 | 22 | AAH93828 | Human prostate-spe |
| c | 116 | 32 | 2.1 | 6082 | 22 | AAH85142 | Human prostate-spe |
| c | 117 | 32 | 2.1 | 6082 | 24 | ABL95292 | Human P510S cDNA s |
| c | 118 | 32 | 2.1 | 6338 | 18 | AAT91384 | Vector pcDNA3-IgG1 |
| c | 119 | 32 | 2.1 | 6338 | 20 | AAZ30851 | Murine IgG1 heavy |
| c | 120 | 32 | 2.1 | 6338 | 21 | AAZ87246 | Plasmid pcDNA3-IgG |
| c | 121 | 32 | 2.1 | 6404 | 21 | AAC61514 | Nucleotide sequenc |
| c | 122 | 32 | 2.1 | 6439 | 24 | AAS16715 | Plasmid pOut-cre. |
| c | 123 | 32 | 2.1 | 6452 | 24 | AAS16714 | Plasmid pOut-flp. |
| c | 124 | 32 | 2.1 | 6801 | 22 | AAD06056 | Plasmid LBDASNLSVP |
| c | 125 | 32 | 2.1 | 6801 | 22 | AAD06059 | Plasmid C7LBDBSVP1 |
| c | 126 | 32 | 2.1 | 6980 | 22 | AAH47043 | Nucleotide sequenc |
| c | 127 | 32 | 2.1 | 7076 | 24 | AAS16709 | Plasmid pFastFind- |
| c | 128 | 32 | 2.1 | 7076 | 24 | AAS16710 | Plasmid pFastFind- |
| c | 129 | 32 | 2.1 | 7092 | 24 | AAS16708 | Plasmid pFastFind- |
| c | 130 | 32 | 2.1 | 7092 | 24 | AAS16711 | Plasmid pFastFind- |
| c | 131 | 32 | 2.1 | 7108 | 20 | AAX02662 | EP-892047 Seq ID 3 |
| c | 132 | 32 | 2.1 | 7469 | 22 | AAH47042 | Nucleotide sequenc |
| c | 133 | 32 | 2.1 | 7563 | 22 | AAH47041 | Nucleotide sequenc |
| c | 134 | 32 | 2.1 | 7573 | 24 | AAS16716 | Plasmid pFastFind- |
| | 135 | 32 | 2.1 | 7648 | 22 | AAH48763 | Vector pHA-Ub DNA. |
| c | 136 | 32 | 2.1 | 13928 | 22 | AAH77500 | Haemophilia B gene |
| | 137 | 31 | 2.1 | 40 | 16 | AAQ99121 | Oligo 173. Synthe |
| c | 138 | 31 | 2.1 | 400 | 22 | AAS13858 | Triple carbohydrat |
| | 139 | 31 | 2.1 | 400 | 22 | AAS13859 | Triple carbohydrat |
| c | 140 | 31 | 2.1 | 489 | 22 | AAS13861 | Actin response ele |
| c | 141 | 31 | 2.1 | 1210 | 24 | ABK69065 | DNA encoding human |
| | 142 | 31 | 2.1 | 1584 | 22 | AAF23419 | Human SEC10 DNA se |
| c | 143 | 31 | 2.1 | 2053 | 24 | ABK49911 | cDNA encoding huma |
| c | 144 | 31 | 2.1 | 6420 | 21 | AAC61515 | Nucleotide sequenc |
| c | 145 | 31 | 2.1 | 6795 | 21 | AAC66817 | Reporter gene cons |
| c | 146 | 31 | 2.1 | 6795 | 21 | AAC66821 | Reporter gene cons |
| c | 147 | 31 | 2.1 | 6795 | 21 | AAC66822 | Reporter gene cons |
| c | 148 | 31 | 2.1 | 8637 | 21 | AAC66818 | Reporter gene cons |
| c | 149 | 30 | 2.0 | 33 | 22 | AAD20338 | PCR primer, CAB2H3 |
| c | 150 | 30 | 2.0 | 33 | 22 | AAD08153 | PCR primer CAB2H3- |
| c | 151 | 30 | 2.0 | 33 | 24 | AAD27291 | PCR primer, CAB2H3 |
| c | 152 | 30 | 2.0 | 245 | 21 | AAA14578 | Partial sequence o |
| c | 153 | 30 | 2.0 | 249 | 21 | AAA14577 | Partial sequence o |
| c | 154 | 30 | 2.0 | 250 | 21 | AAA14576 | Partial sequence o |
| c | 155 | 30 | 2.0 | 258 | 21 | AAA14570 | Sequence map of a |
| c | 156 | 30 | 2.0 | 281 | 21 | AAA14579 | Partial sequence o |
| c | 157 | 30 | 2.0 | 686 | 23 | AAD23532 | Human lung tumour- |
| c | 158 | 29 | 1.9 | 34 | 16 | AAQ99122 | Oligo 174. Synthe |
| | 159 | 29 | 1.9 | 66 | 20 | AAZ25380 | Human FLINT PCR pr |
| | 160 | 29 | 1.9 | 66 | 21 | AAA51080 | Reverse primer for |
| c | 161 | 27 | 1.8 | 5458 | 24 | ABL58493 | Recombinant vector |
| c | 162 | 27 | 1.8 | 5458 | 24 | ABL58494 | Recombinant vector |
| c | 163 | 27 | 1.8 | 5614 | 24 | ABL58489 | Recombinant vector |
| c | 164 | 27 | 1.8 | 5614 | 24 | ABL58490 | Recombinant vector |
| | 165 | 26 | 1.7 | 33 | 16 | AAQ87502 | DAF-N2 PCR primer. |
| | 166 | 26 | 1.7 | 33 | 20 | AAX25330 | Human TNF receptor |
| | 167 | 26 | 1.7 | 57 | 24 | ABK16235 | Human lung tumour |
| | 168 | 25 | 1.7 | 39 | 16 | AAQ87497 | DAF-N5 PCR primer. |
| c | 169 | 25 | 1.7 | 40 | 19 | AAV33370 | Prolactin leader s |
| | 170 | 25 | 1.7 | 45 | 19 | AAV33391 | Nucleotide sequenc |
| | 171 | 25 | 1.7 | 54 | 20 | AAX84484 | PCR primer for mur |
| | 172 | 25 | 1.7 | 56 | 19 | AAV04955 | Antisense primer u |
| c | 173 | 25 | 1.7 | 56 | 21 | AAA90580 | PHA-MCL 5' PCR pri |
| | 174 | 25 | 1.7 | 57 | 21 | AAA48678 | PCR primer FLAGM1. |
| c | 175 | 25 | 1.7 | 57 | 22 | AAF87699 | FLAG epitope tag c |
| | 176 | 25 | 1.7 | 59 | 20 | AAX87864 | Human fibrinogen d |
| | 177 | 25 | 1.7 | 59 | 24 | AAD22570 | Human FDRG flag ep |
| | 178 | 25 | 1.7 | 60 | 20 | AAX08402 | PCR primer used fo |
| | 179 | 25 | 1.7 | 62 | 21 | AAA64961 | Protein scaffold m |
| | 180 | 25 | 1.7 | 62 | 22 | AAD16978 | Oligonucleotide HF |
| | 181 | 25 | 1.7 | 62 | 24 | ABN87085 | Human 10 Fn3 gene |
| | 182 | 25 | 1.7 | 64 | 21 | AAA64964 | Protein scaffold m |
| | 183 | 25 | 1.7 | 64 | 22 | AAD16981 | Oligonucleotide HF |
| | 184 | 25 | 1.7 | 64 | 24 | ABN87088 | Human 10 Fn3 gene |
| c | 185 | 25 | 1.7 | 64 | 24 | ABK55211 | Human colon cancer |
| | 186 | 25 | 1.7 | 72 | 20 | AAZ29923 | PCR primer MAL2 us |
| | 187 | 25 | 1.7 | 108 | 22 | AAD16977 | Oligonucleotide HF |
| | 188 | 25 | 1.7 | 123 | 22 | AAD16980 | Oligonucleotide HF |
| | 189 | 25 | 1.7 | 126 | 21 | AAA64960 | Protein scaffold m |
| | 190 | 25 | 1.7 | 126 | 24 | ABN87084 | Human 10 Fn3 gene |
| | 191 | 25 | 1.7 | 132 | 21 | AAA64963 | Protein scaffold m |
| | 192 | 25 | 1.7 | 132 | 24 | ABN87087 | Human 10 Fn3 gene |
| c | 193 | 25 | 1.7 | 238 | 18 | AAT84523 | hPSTI.M2 gene for |
| c | 194 | 25 | 1.7 | 446 | 22 | AAS56479 | Human cDNA for an |
| c | 195 | 25 | 1.7 | 480 | 18 | AAT48441 | TGF-beta-like cyto |
| c | 196 | 25 | 1.7 | 513 | 18 | AAT48450 | TGF-beta-like cyto |
| c | 197 | 25 | 1.7 | 633 | 20 | AAV72021 | Adenovirus T5sigDE |
| c | 198 | 25 | 1.7 | 960 | 20 | AAV72020 | Adenovirus T5S7sig |
| c | 199 | 25 | 1.7 | 1300 | 19 | AAV33371 | PROLAC FLAG-connec |
| c | 200 | 25 | 1.7 | 1300 | 19 | AAV33372 | PROLAC FLAG-connec |
| c | 201 | 25 | 1.7 | 1369 | 19 | AAV42918 | Truncated Interleu |
| c | 202 | 25 | 1.7 | 1408 | 24 | ABL58244 | Human transferase |
| | 203 | 25 | 1.7 | 1461 | 21 | AAC45069 | Arabidopsis thalia |
| | 204 | 25 | 1.7 | 1466 | 21 | AAC39476 | Arabidopsis thalia |
| c | 205 | 25 | 1.7 | 1704 | 20 | AAV72022 | Adenovirus pACTSsi |
| | 206 | 25 | 1.7 | 2350 | 24 | ABK30270 | Human G-protein-co |
| c | 207 | 25 | 1.7 | 6926 | 18 | AAV04431 | Vector pcDNA3-IgG1 |
| c | 208 | 24 | 1.6 | 24 | 22 | AAF28075 | Nascent protein de |
| c | 209 | 24 | 1.6 | 32 | 22 | AAC83694 | Forward primer use |
| | 210 | 24 | 1.6 | 33 | 21 | AAA64969 | Protein scaffold m |
| c | 211 | 24 | 1.6 | 33 | 22 | AAI65561 | PCR primer used to |
| | 212 | 24 | 1.6 | 33 | 22 | AAI65562 | PCR primer used to |
| | 213 | 24 | 1.6 | 33 | 22 | AAD16986 | Oligonucleotide AS |
| | 214 | 24 | 1.6 | 33 | 24 | ABN87093 | ASAflag8 oligonucl |
| c | 215 | 24 | 1.6 | 35 | 7 | AAN60031 | Sequence encoding |
| c | 216 | 24 | 1.6 | 36 | 22 | AAC83696 | Forward PCR primer |
| c | 217 | 24 | 1.6 | 45 | 16 | AAQ87498 | DAF-C5 PCR primer. |
| c | 218 | 24 | 1.6 | 45 | 22 | AAF84413 | PCR primer SX-FLAG |
| | 219 | 24 | 1.6 | 45 | 22 | AAF84414 | PCR primer SX-FLAG |
| | 220 | 24 | 1.6 | 54 | 20 | AAX86457 | PCR primer used to |
| c | 221 | 24 | 1.6 | 54 | 21 | AAA49880 | Plasmid pCR3.1 mul |
| c | 222 | 24 | 1.6 | 54 | 21 | AAZ61088 | Forward PCR primer |
| | 223 | 24 | 1.6 | 57 | 21 | AAA64967 | Protein scaffold m |
| | 224 | 24 | 1.6 | 57 | 22 | AAD16984 | Oligonucleotide HF |
| | 225 | 24 | 1.6 | 57 | 24 | ABN87091 | Human 10 Fn3 gene |
| | 226 | 24 | 1.6 | 58 | 21 | AAZ39001 | Human DNA fragment |
| | 227 | 24 | 1.6 | 58 | 22 | AAH74651 | PCR primer for cDN |
| | 228 | 24 | 1.6 | 58 | 22 | AAD02507 | Human DFF40 coding |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 229 | 24 | 1.6 | 58 | 22 | AAD02515 | Alternative versio |
| | 230 | 24 | 1.6 | 59 | 18 | AAT45831 | Hepatitis GB virus |
| c | 231 | 24 | 1.6 | 59 | 22 | AAF82659 | Primer used to con |
| | 232 | 24 | 1.6 | 60 | 18 | AAT45832 | Hepatitis GB virus |
| | 233 | 24 | 1.6 | 63 | 18 | AAT45852 | Hepatitis GB virus |
| | 234 | 24 | 1.6 | 66 | 24 | ABK84822 | Human G protein-co |
| | 235 | 24 | 1.6 | 66 | 24 | ABK70637 | Human G-protein co |
| | 236 | 24 | 1.6 | 69 | 20 | AAZ10739 | PCR primer used to |
| | 237 | 24 | 1.6 | 69 | 24 | ABK43270 | Human HKNG1 cDNA/F |
| c | 238 | 24 | 1.6 | 72 | 22 | AAD16125 | D3SD3-FLAG-His6 ta |
| c | 239 | 24 | 1.6 | 106 | 22 | AAD20354 | PCR primer, CAB4-3 |
| c | 240 | 24 | 1.6 | 106 | 22 | AAD08169 | Primer CAB4-33P fo |
| c | 241 | 24 | 1.6 | 106 | 24 | AAD27307 | Primer, CAB4-33P t |
| | 242 | 24 | 1.6 | 114 | 21 | AAA64966 | Protein scaffold m |
| | 243 | 24 | 1.6 | 114 | 22 | AAD16983 | Oligonucleotide HF |
| | 244 | 24 | 1.6 | 114 | 24 | ABN87090 | Human 10 Fn3 gene |
| c | 245 | 24 | 1.6 | 141 | 22 | AAS00954 | A segment of expre |
| | 246 | 24 | 1.6 | 978 | 20 | AAZ30974 | Porcine complement |
| c | 247 | 23 | 1.5 | 30 | 24 | ABL52525 | Human DAF PCR prim |
| c | 248 | 23 | 1.5 | 36 | 15 | AAQ58217 | Synthetic FLAG seq |
| c | 249 | 23 | 1.5 | 39 | 22 | AAD20351 | PCR primer, DAFSXB |
| c | 250 | 23 | 1.5 | 266 | 21 | AAA74208 | Loblolly pine SSR |
| c | 251 | 23 | 1.5 | 1590 | 19 | AAV19125 | Nucleotide sequenc |
| c | 252 | 23 | 1.5 | 1590 | 20 | AAX25066 | Brassica napus lyc |
| c | 253 | 23 | 1.5 | 1590 | 24 | ABA97357 | Brassica napus bet |
| c | 254 | 23 | 1.5 | 10172 | 22 | AAD21290 | Human phospholipas |
| c | 255 | 23 | 1.5 | 13104 | 14 | AAQ46852 | Clone of recombina |
| c | 256 | 23 | 1.5 | 31068 | 23 | ABL28588 | Drosophila melanog |
| | 257 | 22 | 1.5 | 22 | 19 | AAV54662 | Complement DAF mRN |
| | 258 | 22 | 1.5 | 23 | 21 | AAZ48624 | PCR primer for hum |
| | 259 | 22 | 1.5 | 28 | 15 | AAQ58889 | Primer for amplify |
| c | 260 | 22 | 1.5 | 30 | 21 | AAC87810 | Zymogen activation |
| c | 261 | 22 | 1.5 | 30 | 22 | AAF55284 | Primer used to pro |
| c | 262 | 22 | 1.5 | 31 | 16 | AAQ87503 | DAF-C2R PCR primer |
| c | 263 | 22 | 1.5 | 33 | 15 | AAQ58883 | Primer for amplify |
| c | 264 | 22 | 1.5 | 45 | 21 | AAC87821 | Zymogen activation |
| c | 265 | 22 | 1.5 | 45 | 22 | AAF55295 | Primer used to pro |
| c | 266 | 22 | 1.5 | 47 | 16 | AAQ99116 | cCIP DC oligo 55 - |
| c | 267 | 22 | 1.5 | 49 | 22 | AAH43432 | Primer J NS2 Forw |
| | 268 | 22 | 1.5 | 53 | 21 | AAC87822 | Zymogen activation |
| | 269 | 22 | 1.5 | 53 | 22 | AAF55296 | Primer used to pro |
| c | 270 | 22 | 1.5 | 158 | 11 | AAQ03349 | High level express |
| c | 271 | 22 | 1.5 | 352 | 21 | AAC87793 | Activation constru |
| c | 272 | 22 | 1.5 | 352 | 22 | AAF55265 | Nucleotide sequenc |
| c | 273 | 22 | 1.5 | 361 | 21 | AAC87789 | Activation constru |
| c | 274 | 22 | 1.5 | 361 | 22 | AAF55261 | Nucleotide sequenc |
| c | 275 | 22 | 1.5 | 382 | 21 | AAC87792 | Activation constru |
| c | 276 | 22 | 1.5 | 382 | 22 | AAF55264 | Nucleotide sequenc |
| c | 277 | 22 | 1.5 | 385 | 21 | AAC87794 | Activation constru |
| c | 278 | 22 | 1.5 | 385 | 22 | AAF55266 | Nucleotide sequenc |
| c | 279 | 22 | 1.5 | 424 | 22 | AAS56499 | Human cDNA for an |
| | 280 | 22 | 1.5 | 479 | 22 | ABA42091 | Human breast cell |
| | 281 | 22 | 1.5 | 479 | 22 | ABA52513 | Human foetal liver |
| | 282 | 22 | 1.5 | 479 | 22 | ABA22302 | Probe #768 for gen |
| | 283 | 22 | 1.5 | 479 | 22 | AAK00777 | Human brain expres |
| | 284 | 22 | 1.5 | 479 | 22 | AAK26229 | Human bone marrow |
| | 285 | 22 | 1.5 | 479 | 22 | AAI10862 | Probe #795 for gen |
| | 286 | 22 | 1.5 | 479 | 22 | AAI32122 | Probe #808 used to |
| | 287 | 22 | 1.5 | 479 | 22 | AAI00786 | Probe #777 used to |
| | 288 | 22 | 1.5 | 479 | 24 | ABS00817 | Human genome-deriv |
| c | 289 | 22 | 1.5 | 484 | 21 | AAC87791 | Activation constru |
| c | 290 | 22 | 1.5 | 484 | 22 | AAF55263 | Nucleotide sequenc |
| c | 291 | 22 | 1.5 | 807 | 24 | ABK55431 | Human colon cancer |
| | 292 | 22 | 1.5 | 830 | 22 | ABA49206 | Human breast cell |
| | 293 | 22 | 1.5 | 830 | 22 | ABA67121 | Human foetal liver |
| | 294 | 22 | 1.5 | 830 | 22 | ABA34211 | Probe #12677 for g |
| | 295 | 22 | 1.5 | 830 | 22 | AAK15561 | Human brain expres |
| | 296 | 22 | 1.5 | 830 | 22 | AAK41294 | Human bone marrow |
| | 297 | 22 | 1.5 | 830 | 22 | AAI22045 | Probe #11978 for g |
| | 298 | 22 | 1.5 | 830 | 22 | AAI47337 | Probe #16023 used |
| | 299 | 22 | 1.5 | 830 | 22 | AAI07740 | Probe #7731 used t |
| | 300 | 22 | 1.5 | 830 | 24 | ABS15303 | Human genome-deriv |
| | 301 | 22 | 1.5 | 893 | 24 | AAS62424 | cDNA sequence #211 |
| c | 302 | 22 | 1.5 | 1037 | 22 | AAF55272 | Nucleotide sequenc |
| c | 303 | 22 | 1.5 | 1049 | 21 | AAC87797 | Activation constru |
| c | 304 | 22 | 1.5 | 1049 | 22 | AAF55269 | Nucleotide sequenc |
| c | 305 | 22 | 1.5 | 1052 | 21 | AAC87798 | Activation constru |
| c | 306 | 22 | 1.5 | 1052 | 22 | AAF55270 | Nucleotide sequenc |
| c | 307 | 22 | 1.5 | 1103 | 22 | AAF55271 | Nucleotide sequenc |
| c | 308 | 22 | 1.5 | 1130 | 22 | AAS01366 | Recombinant human |
| c | 309 | 22 | 1.5 | 1130 | 22 | AAF77000 | Fusion gene of pro |
| c | 310 | 22 | 1.5 | 1142 | 21 | AAC87796 | Activation constru |
| c | 311 | 22 | 1.5 | 1142 | 22 | AAF55268 | Nucleotide sequenc |
| c | 312 | 22 | 1.5 | 1166 | 22 | AAD02991 | Zymogen activation |
| c | 313 | 22 | 1.5 | 1169 | 21 | AAC87795 | Activation constru |
| c | 314 | 22 | 1.5 | 1169 | 22 | AAF55267 | Nucleotide sequenc |
| c | 315 | 22 | 1.5 | 1189 | 24 | AAI64290 | Protease D-G catay |
| c | 316 | 22 | 1.5 | 1550 | 21 | AAA57955 | 1550 bp Candida al |
| c | 317 | 22 | 1.5 | 2027 | 21 | AAA58002 | 2027 bp Candida al |
| c | 318 | 22 | 1.5 | 2190 | 24 | AAS18067 | Ashbya gossypii AG |
| c | 319 | 22 | 1.5 | 4510 | 23 | ABL20209 | Drosophila melanog |
| c | 320 | 22 | 1.5 | 4785 | 23 | ABL13743 | Drosophila melanog |
| c | 321 | 22 | 1.5 | 4852 | 23 | ABL09963 | Drosophila melanog |
| c | 322 | 22 | 1.5 | 6140 | 22 | AAS63922 | Human prostate cDN |
| c | 323 | 22 | 1.5 | 6140 | 22 | AAH93829 | Human prostate-spe |
| c | 324 | 22 | 1.5 | 6140 | 22 | AAH85143 | Human prostate-spe |
| c | 325 | 22 | 1.5 | 6140 | 24 | ABL95293 | Human P510S cDNA s |
| c | 326 | 22 | 1.5 | 6147 | 24 | AAL45982 | Plasmid pSMICIP2s( |
| | 327 | 22 | 1.5 | 6637 | 23 | ABL15520 | Drosophila melanog |
| c | 328 | 22 | 1.5 | 7005 | 23 | ABL15355 | Drosophila melanog |
| c | 329 | 22 | 1.5 | 8749 | 22 | AAH47044 | Nucleotide sequenc |
| c | 330 | 22 | 1.5 | 13075 | 23 | ABL15354 | Drosophila melanog |
| c | 331 | 22 | 1.5 | 22788 | 23 | ABL20208 | Drosophila melanog |
| c | 332 | 22 | 1.5 | 44456 | 23 | ABL09962 | Drosophila melanog |
| c | 333 | 22 | 1.5 | 49431 | 23 | ABL13742 | Drosophila melanog |
| c | 334 | 22 | 1.5 | 325791 | 22 | AAS43104 | Human Oestrogen re |
| c | 335 | 21 | 1.4 | 21 | 20 | AAX87918 | Human tumour assoc |
| | 336 | 21 | 1.4 | 22 | 24 | ABK95214 | PCR primer contain |
| | 337 | 21 | 1.4 | 28 | 14 | AAQ41910 | erb B2/neu promote |
| | 338 | 21 | 1.4 | 28 | 24 | ABK95215 | PCR primer contain |
| | 339 | 21 | 1.4 | 34 | 24 | ABK95216 | PCR primer contain |
| | 340 | 21 | 1.4 | 39 | 19 | AAV39018 | GnT-IV cDNA contai |
| | 341 | 21 | 1.4 | 39 | 19 | AAV39021 | GnT-IV cDNA contai |
| | 342 | 21 | 1.4 | 40 | 24 | ABK95217 | PCR primer contain |
| | 343 | 21 | 1.4 | 41 | 14 | AAQ41909 | erb B2/neu promote |
| | 344 | 21 | 1.4 | 41 | 15 | AAQ55568 | Sequence of synthe |
| | 345 | 21 | 1.4 | 41 | 15 | AAQ55567 | Sequence of synthe |
| | 346 | 21 | 1.4 | 41 | 15 | AAQ67228 | Triple helix-formi |
| | 347 | 21 | 1.4 | 45 | 21 | AAZ90037 | Reverse PCR primer |
| | 348 | 21 | 1.4 | 47 | 24 | ABK95211 | PCR primer contain |
| c | 349 | 21 | 1.4 | 51 | 24 | ABL60621 | Nucleotide fragmen |
| c | 350 | 21 | 1.4 | 51 | 24 | ABK10896 | DNA encoding polya |
| | 351 | 21 | 1.4 | 52 | 22 | AAH78170 | Nucleotide sequenc |
| | 352 | 21 | 1.4 | 52 | 24 | ABK71349 | Thrombopoietin (TP |
| | 353 | 21 | 1.4 | 52 | 24 | ABA04546 | PCR primer #24. S |
| | 354 | 21 | 1.4 | 54 | 14 | AAQ41908 | erb B2/neu promote |
| | 355 | 21 | 1.4 | 54 | 20 | AAX08406 | PCR primer used fo |
| c | 356 | 21 | 1.4 | 54 | 24 | AAS96056 | Leishmania antigen |
| c | 357 | 21 | 1.4 | 59 | 21 | AAA29363 | PCR primer 55-101. |
| c | 358 | 21 | 1.4 | 59 | 24 | ABA99070 | Sorangium cellulos |
| | 359 | 21 | 1.4 | 93 | 21 | AAA51730 | PTH functional dom |
| c | 360 | 21 | 1.4 | 121 | 24 | ABK25389 | Male-sterile plant |
| | 361 | 21 | 1.4 | 121 | 24 | ABK25390 | Male-sterile plant |
| c | 362 | 21 | 1.4 | 121 | 24 | ABK25393 | Male-sterile plant |
| | 363 | 21 | 1.4 | 121 | 24 | ABK25394 | Male-sterile plant |
| c | 364 | 21 | 1.4 | 148 | 22 | ABA48927 | Human breast cell |
| c | 365 | 21 | 1.4 | 148 | 22 | ABA66842 | Human foetal liver |
| c | 366 | 21 | 1.4 | 148 | 22 | ABA33909 | Probe #12375 for g |
| c | 367 | 21 | 1.4 | 148 | 22 | AAK15273 | Human brain expres |
| c | 368 | 21 | 1.4 | 148 | 22 | AAK40999 | Human bone marrow |
| c | 369 | 21 | 1.4 | 148 | 22 | AAI21768 | Probe #11701 for g |
| c | 370 | 21 | 1.4 | 148 | 22 | AAI47050 | Probe #15736 used |
| c | 371 | 21 | 1.4 | 148 | 22 | AAI07454 | Probe #7445 used t |
| c | 372 | 21 | 1.4 | 148 | 24 | ABS14969 | Human genome-deriv |
| | 373 | 21 | 1.4 | 203 | 22 | ABA46770 | Human breast cell |
| | 374 | 21 | 1.4 | 203 | 22 | ABA47327 | Human breast cell |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 375 | 21 | 1.4 | 203 | 22 | ABA64650 | Human foetal liver |
| | 376 | 21 | 1.4 | 203 | 22 | ABA65212 | Human foetal liver |
| | 377 | 21 | 1.4 | 203 | 22 | ABA31776 | Probe #10242 for g |
| | 378 | 21 | 1.4 | 203 | 22 | ABA32313 | Probe #10779 for g |
| | 379 | 21 | 1.4 | 203 | 22 | AAK13088 | Human brain expres |
| | 380 | 21 | 1.4 | 203 | 22 | AAK13629 | Human brain expres |
| | 381 | 21 | 1.4 | 203 | 22 | AAK38816 | Human bone marrow |
| | 382 | 21 | 1.4 | 203 | 22 | AAK39370 | Human bone marrow |
| | 383 | 21 | 1.4 | 203 | 22 | AAI19624 | Probe #9557 for ge |
| | 384 | 21 | 1.4 | 203 | 22 | AAI20183 | Probe #10116 for g |
| | 385 | 21 | 1.4 | 203 | 22 | AAI44820 | Probe #13506 used |
| | 386 | 21 | 1.4 | 203 | 22 | AAI45383 | Probe #14069 used |
| | 387 | 21 | 1.4 | 203 | 22 | AAI05343 | Probe #5334 used t |
| | 388 | 21 | 1.4 | 203 | 22 | AAI05887 | Probe #5878 used t |
| | 389 | 21 | 1.4 | 203 | 24 | ABS12897 | Human genome-deriv |
| | 390 | 21 | 1.4 | 203 | 24 | ABS13457 | Human genome-deriv |
| | 391 | 21 | 1.4 | 324 | 22 | AAK54243 | Murine transport a |
| | 392 | 21 | 1.4 | 329 | 16 | AAQ95203 | Simple tandem repe |
| c | 393 | 21 | 1.4 | 364 | 22 | AAI80186 | Human polynucleoti |
| c | 394 | 21 | 1.4 | 369 | 21 | AAA31283 | Plant microsatelli |
| | 395 | 21 | 1.4 | 372 | 23 | ABV16193 | Human prostate exp |
| c | 396 | 21 | 1.4 | 381 | 22 | ABA43823 | Human breast cell |
| c | 397 | 21 | 1.4 | 381 | 22 | ABA54279 | Human foetal liver |
| c | 398 | 21 | 1.4 | 381 | 22 | ABA24034 | Probe #2500 for ge |
| c | 399 | 21 | 1.4 | 381 | 22 | AAK02558 | Human brain expres |
| c | 400 | 21 | 1.4 | 381 | 22 | AAK27997 | Human bone marrow |
| c | 401 | 21 | 1.4 | 381 | 22 | AAI12579 | Probe #2512 for ge |
| c | 402 | 21 | 1.4 | 381 | 22 | AAI33926 | Probe #2612 used t |
| c | 403 | 21 | 1.4 | 381 | 22 | AAI02485 | Probe #2476 used t |
| c | 404 | 21 | 1.4 | 381 | 24 | ABS02467 | Human genome-deriv |
| c | 405 | 21 | 1.4 | 392 | 21 | AAA31516 | Plant microsatelli |
| | 406 | 21 | 1.4 | 412 | 23 | ABV45991 | Human prostate exp |
| c | 407 | 21 | 1.4 | 435 | 21 | AAC56072 | Eucalyptus grandis |
| c | 408 | 21 | 1.4 | 439 | 21 | AAA31249 | Plant microsatelli |
| c | 409 | 21 | 1.4 | 442 | 22 | AAL34937 | Human musculoskele |
| | 410 | 21 | 1.4 | 448 | 20 | AAZ33729 | Tobacco plant resi |
| | 411 | 21 | 1.4 | 453 | 22 | ABA51994 | Human foetal liver |
| | 412 | 21 | 1.4 | 453 | 22 | ABA21810 | Probe #276 for gen |
| | 413 | 21 | 1.4 | 453 | 22 | AAK00280 | Human brain expres |
| | 414 | 21 | 1.4 | 453 | 22 | AAK25720 | Human bone marrow |
| | 415 | 21 | 1.4 | 453 | 22 | AAI10349 | Probe #282 for gen |
| | 416 | 21 | 1.4 | 453 | 22 | AAI31602 | Probe #288 used to |
| | 417 | 21 | 1.4 | 453 | 22 | AAI00284 | Probe #275 used to |
| | 418 | 21 | 1.4 | 453 | 24 | ABS00300 | Human genome-deriv |
| | 419 | 21 | 1.4 | 471 | 22 | ABA42176 | Human breast cell |
| | 420 | 21 | 1.4 | 471 | 22 | ABA52598 | Human foetal liver |
| | 421 | 21 | 1.4 | 471 | 22 | ABA22386 | Probe #852 for gen |
| | 422 | 21 | 1.4 | 471 | 22 | AAK00859 | Human brain expres |
| | 423 | 21 | 1.4 | 471 | 22 | AAK26314 | Human bone marrow |
| | 424 | 21 | 1.4 | 471 | 22 | AAI10947 | Probe #880 for gen |
| | 425 | 21 | 1.4 | 471 | 22 | AAI32207 | Probe #893 used to |
| | 426 | 21 | 1.4 | 471 | 22 | AAI00868 | Probe #859 used to |
| | 427 | 21 | 1.4 | 471 | 24 | ABS00902 | Human genome-deriv |
| c | 428 | 21 | 1.4 | 538 | 21 | AAC09682 | Human secreted pro |
| c | 429 | 21 | 1.4 | 549 | 23 | ABL27301 | Drosophila melanog |
| | 430 | 21 | 1.4 | 660 | 24 | ABQ44606 | Oligonucleotide fo |
| c | 431 | 21 | 1.4 | 660 | 24 | ABQ44607 | Oligonucleotide fo |
| | 432 | 21 | 1.4 | 672 | 15 | AAQ70140 | Cadrac cDNA. Homo |
| | 433 | 21 | 1.4 | 675 | 24 | ABQ65806 | Arabidopsis thalia |
| | 434 | 21 | 1.4 | 700 | 21 | AAA37652 | FMR1 gene variable |
| | 435 | 21 | 1.4 | 874 | 24 | ABQ22614 | Oligonucleotide fo |
| c | 436 | 21 | 1.4 | 874 | 24 | ABQ22615 | Oligonucleotide fo |
| | 437 | 21 | 1.4 | 877 | 24 | ABQ29262 | Oligonucleotide fo |
| c | 438 | 21 | 1.4 | 877 | 24 | ABQ29263 | Oligonucleotide fo |
| | 439 | 21 | 1.4 | 887 | 22 | ABA51240 | Human breast cell |
| | 440 | 21 | 1.4 | 887 | 22 | ABA69248 | Human foetal liver |
| | 441 | 21 | 1.4 | 887 | 22 | ABA36164 | Probe #14630 for g |
| | 442 | 21 | 1.4 | 887 | 22 | AAK17542 | Human brain expres |
| | 443 | 21 | 1.4 | 887 | 22 | AAK43350 | Human bone marrow |
| | 444 | 21 | 1.4 | 887 | 22 | AAI24125 | Probe #14058 for g |
| | 445 | 21 | 1.4 | 887 | 22 | AAI49421 | Probe #18107 used |
| | 446 | 21 | 1.4 | 887 | 22 | AAI09699 | Probe #9690 used t |
| | 447 | 21 | 1.4 | 887 | 24 | ABS17431 | Human genome-deriv |
| c | 448 | 21 | 1.4 | 895 | 10 | AAN91051 | Sequence encoding |
| c | 449 | 21 | 1.4 | 895 | 11 | AAQ05087 | Sequence encoding |
| c | 450 | 21 | 1.4 | 1054 | 24 | ABK65201 | Arabidopsis cDNA e |
| c | 451 | 21 | 1.4 | 1148 | 22 | AAS26350 | Human cDNA encodin |
| c | 452 | 21 | 1.4 | 1179 | 22 | AAS25897 | Human cDNA encodin |
| c | 453 | 21 | 1.4 | 1329 | 21 | AAA80677 | Human secreted pro |
| | 454 | 21 | 1.4 | 1359 | 21 | AAC44705 | Arabidopsis thalia |
| | 455 | 21 | 1.4 | 1386 | 23 | AAS76635 | DNA encoding novel |
| c | 456 | 21 | 1.4 | 1413 | 20 | AAX80055 | Human PRO355 nucle |
| c | 457 | 21 | 1.4 | 1413 | 21 | AAA49563 | Human PRO355 cDNA. |
| c | 458 | 21 | 1.4 | 1413 | 22 | AAS45941 | Human DNA encoding |
| c | 459 | 21 | 1.4 | 1500 | 21 | AAA27051 | Human cell surface |
| c | 460 | 21 | 1.4 | 1507 | 22 | AAH98350 | Human EST-derived |
| c | 461 | 21 | 1.4 | 1508 | 21 | AAA80623 | Human secreted pro |
| c | 462 | 21 | 1.4 | 1520 | 21 | AAA80616 | Human secreted pro |
| | 463 | 21 | 1.4 | 1592 | 23 | ABL27300 | Drosophila melanog |
| c | 464 | 21 | 1.4 | 1598 | 21 | AAZ50882 | Human lymphoid der |
| c | 465 | 21 | 1.4 | 1605 | 21 | AAA29166 | Catalpa 4-hydroxyp |
| c | 466 | 21 | 1.4 | 1638 | 12 | AAQ13656 | Encodes human brai |
| c | 467 | 21 | 1.4 | 1721 | 14 | AAQ54257 | APP-REP 751 amyloi |
| | 468 | 21 | 1.4 | 1776 | 21 | AAA71636 | Human aspartate pr |
| c | 469 | 21 | 1.4 | 1910 | 21 | AAC41791 | Arabidopsis thalia |
| | 470 | 21 | 1.4 | 1981 | 22 | ABA46128 | Human breast cell |
| | 471 | 21 | 1.4 | 1981 | 22 | ABA56674 | Human foetal liver |
| | 472 | 21 | 1.4 | 1981 | 22 | ABA26279 | Probe #4745 for ge |
| | 473 | 21 | 1.4 | 1981 | 22 | AAK04811 | Human brain expres |
| | 474 | 21 | 1.4 | 1981 | 22 | AAK30333 | Human bone marrow |
| | 475 | 21 | 1.4 | 1981 | 22 | AAI14937 | Probe #4870 for ge |
| | 476 | 21 | 1.4 | 1981 | 22 | AAI36292 | Probe #4978 used t |
| | 477 | 21 | 1.4 | 1981 | 22 | AAI04714 | Probe #4705 used t |
| | 478 | 21 | 1.4 | 1981 | 24 | ABS04920 | Human genome-deriv |
| c | 479 | 21 | 1.4 | 2085 | 15 | AAQ69003 | Mouse amyloid prec |
| c | 480 | 21 | 1.4 | 2088 | 13 | AAQ27801 | APP695. Homo sapi |
| c | 481 | 21 | 1.4 | 2088 | 20 | AAX57707 | Amyloid precursor |
| c | 482 | 21 | 1.4 | 2088 | 21 | AAA15671 | Human APP695 nucle |
| c | 483 | 21 | 1.4 | 2088 | 21 | AAA15672 | Human APP695-sw va |
| c | 484 | 21 | 1.4 | 2088 | 21 | AAA15676 | Human APP695-VF nu |
| c | 485 | 21 | 1.4 | 2088 | 22 | AAD17868 | Human wild-type am |
| c | 486 | 21 | 1.4 | 2088 | 22 | AAD17869 | Human amyloid prot |
| c | 487 | 21 | 1.4 | 2088 | 22 | AAD17870 | Human amyloid prot |
| c | 488 | 21 | 1.4 | 2088 | 22 | AAD13024 | Human wild-type am |
| c | 489 | 21 | 1.4 | 2088 | 22 | AAD13025 | Human amyloid prec |
| c | 490 | 21 | 1.4 | 2088 | 22 | AAD13026 | Human amyloid prec |
| c | 491 | 21 | 1.4 | 2088 | 22 | AAS11520 | Human cDNA encodin |
| c | 492 | 21 | 1.4 | 2088 | 22 | AAS11521 | Human cDNA encodin |
| c | 493 | 21 | 1.4 | 2088 | 22 | AAS11522 | Human cDNA encodin |
| c | 494 | 21 | 1.4 | 2088 | 22 | AAS11706 | DNA encoding human |
| c | 495 | 21 | 1.4 | 2088 | 22 | AAS11707 | DNA encoding human |
| c | 496 | 21 | 1.4 | 2088 | 22 | AAD06742 | Human amyloid prec |
| c | 497 | 21 | 1.4 | 2088 | 22 | AAD06743 | Human amyloid prec |
| c | 498 | 21 | 1.4 | 2088 | 22 | AAD06744 | Human amyloid prec |
| c | 499 | 21 | 1.4 | 2088 | 24 | ABL52460 | Human APP695 nucle |
| c | 500 | 21 | 1.4 | 2088 | 24 | ABL52461 | Human APP695-Sw nu |
| c | 501 | 21 | 1.4 | 2088 | 24 | ABL52462 | Human APP695-VF nu |
| c | 502 | 21 | 1.4 | 2088 | 24 | ABA04088 | Human amyloid prec |
| | 503 | 21 | 1.4 | 2094 | 21 | AAA71623 | Human aspartate pr |
| c | 504 | 21 | 1.4 | 2094 | 21 | AAA15665 | Human APP696-KK nu |
| c | 505 | 21 | 1.4 | 2094 | 21 | AAA15666 | Human APPSW-KK nuc |
| c | 506 | 21 | 1.4 | 2094 | 21 | AAA15667 | Human APP695-VF-KK |
| c | 507 | 21 | 1.4 | 2094 | 22 | AAD17871 | Human amyloid prot |
| c | 508 | 21 | 1.4 | 2094 | 22 | AAD17872 | Human amyloid prot |
| c | 509 | 21 | 1.4 | 2094 | 22 | AAD17873 | Human amyloid prot |
| c | 510 | 21 | 1.4 | 2094 | 22 | AAD13027 | Human amyloid prec |
| c | 511 | 21 | 1.4 | 2094 | 22 | AAD13028 | Human amyloid prec |
| c | 512 | 21 | 1.4 | 2094 | 22 | AAD13029 | Human amyloid prec |
| c | 513 | 21 | 1.4 | 2094 | 22 | AAS11523 | Human cDNA encodin |
| c | 514 | 21 | 1.4 | 2094 | 22 | AAS11524 | Human cDNA encodin |
| c | 515 | 21 | 1.4 | 2094 | 22 | AAS11525 | Human cDNA encodin |
| c | 516 | 21 | 1.4 | 2094 | 22 | AAS11708 | DNA encoding human |
| c | 517 | 21 | 1.4 | 2094 | 22 | AAS11709 | DNA encoding human |
| c | 518 | 21 | 1.4 | 2094 | 22 | AAS11710 | DNA encoding human |
| c | 519 | 21 | 1.4 | 2094 | 22 | AAD06745 | Human amyloid prec |
| c | 520 | 21 | 1.4 | 2094 | 22 | AAD06746 | Human amyloid prec |

| | | | | | | |
|---|---|---|---|---|---|---|
| c 521 | 21 | 1.4 | 2094 | 22 | AAD06747 | Human amyloid prec |
| c 522 | 21 | 1.4 | 2094 | 24 | ABL52463 | Human APP695-KK nu |
| c 523 | 21 | 1.4 | 2094 | 24 | ABL52464 | Human APP695-Sw-KK |
| c 524 | 21 | 1.4 | 2094 | 24 | ABL52465 | Human APP695-VF-KK |
| c 525 | 21 | 1.4 | 2109 | 23 | AAS81477 | DNA encoding novel |
| 526 | 21 | 1.4 | 2143 | 22 | AAI60333 | Human polynucleoti |
| c 527 | 21 | 1.4 | 2154 | 19 | AAX75753 | Human beta-amyloid |
| c 528 | 21 | 1.4 | 2208 | 23 | ABL23887 | Drosophila melanog |
| c 529 | 21 | 1.4 | 2231 | 19 | AAV32556 | Candida albicans C |
| c 530 | 21 | 1.4 | 2253 | 22 | AAD17898 | Human amyloid prot |
| c 531 | 21 | 1.4 | 2253 | 22 | AAD13279 | Human amyloid prec |
| c 532 | 21 | 1.4 | 2253 | 22 | AAS11550 | Human cDNA encodin |
| c 533 | 21 | 1.4 | 2253 | 22 | AAD06771 | Human amyloid prec |
| c 534 | 21 | 1.4 | 2253 | 24 | ABL52490 | Human APP751 nucle |
| c 535 | 21 | 1.4 | 2256 | 9 | AAN80604 | Lambda APCP168i4,a |
| c 536 | 21 | 1.4 | 2256 | 12 | AAQ10014 | Clone lambda APCP1 |
| c 537 | 21 | 1.4 | 2256 | 13 | AAQ20532 | Sequence of clone |
| c 538 | 21 | 1.4 | 2256 | 14 | AAQ42661 | Lambda clone APCP1 |
| c 539 | 21 | 1.4 | 2256 | 20 | AAX77495 | Human beta-amyloid |
| c 540 | 21 | 1.4 | 2259 | 22 | AAD17900 | Human amyloid prot |
| c 541 | 21 | 1.4 | 2259 | 22 | AAD13281 | Human amyloid prec |
| c 542 | 21 | 1.4 | 2259 | 22 | AAS11552 | Human cDNA encodin |
| c 543 | 21 | 1.4 | 2259 | 22 | AAS11737 | DNA encoding human |
| c 544 | 21 | 1.4 | 2259 | 22 | AAD06773 | Human amyloid prec |
| c 545 | 21 | 1.4 | 2259 | 24 | ABL52492 | Human APP751-KK nu |
| c 546 | 21 | 1.4 | 2265 | 13 | AAQ27802 | APP751. Homo sapi |
| c 547 | 21 | 1.4 | 2265 | 20 | AAX08983 | Amyloid precursor |
| 548 | 21 | 1.4 | 2303 | 23 | ABL22388 | Drosophila melanog |
| c 549 | 21 | 1.4 | 2310 | 19 | AAV10322 | Human APP770 cDNA. |
| c 550 | 21 | 1.4 | 2310 | 22 | AAD17897 | Human amyloid prot |
| c 551 | 21 | 1.4 | 2310 | 22 | AAD13278 | Human amyloid prec |
| c 552 | 21 | 1.4 | 2310 | 22 | AAS11549 | Human cDNA encodin |
| c 553 | 21 | 1.4 | 2310 | 22 | AAD06770 | Human amyloid prec |
| c 554 | 21 | 1.4 | 2310 | 24 | ABL52489 | Human APP770 nucle |
| c 555 | 21 | 1.4 | 2310 | 24 | AAK98743 | Polynucleotide seq |
| c 556 | 21 | 1.4 | 2313 | 14 | AAQ48860 | Mutated APP770 exo |
| c 557 | 21 | 1.4 | 2313 | 15 | AAQ74708 | cDNA of APP 770 ge |
| c 558 | 21 | 1.4 | 2313 | 22 | AAD18754 | Human amyloid prec |
| c 559 | 21 | 1.4 | 2316 | 22 | AAD17899 | Human amyloid prot |
| c 560 | 21 | 1.4 | 2316 | 22 | AAD13280 | Human amyloid prec |
| c 561 | 21 | 1.4 | 2316 | 22 | AAS11551 | Human cDNA encodin |
| c 562 | 21 | 1.4 | 2316 | 22 | AAS11736 | DNA encoding human |
| c 563 | 21 | 1.4 | 2316 | 22 | AAD06772 | Human amyloid prec |
| c 564 | 21 | 1.4 | 2316 | 24 | ABL52491 | Human APP770-KK nu |
| c 565 | 21 | 1.4 | 2328 | 23 | AAS84696 | DNA encoding novel |
| 566 | 21 | 1.4 | 2575 | 20 | AAZ10654 | cDNA encoding a hu |
| 567 | 21 | 1.4 | 2584 | 20 | AAZ10676 | cDNA encoding a hu |
| c 568 | 21 | 1.4 | 2605 | 23 | ABL27656 | Drosophila melanog |
| 569 | 21 | 1.4 | 2627 | 22 | AAI58547 | Human polynucleoti |
| c 570 | 21 | 1.4 | 2735 | 24 | AAS96066 | Leishmania antigen |
| c 571 | 21 | 1.4 | 2844 | 23 | ABL09237 | Drosophila melanog |
| c 572 | 21 | 1.4 | 2949 | 10 | AAN91050 | Sequence encoding |
| c 573 | 21 | 1.4 | 2949 | 11 | AAQ05086 | Sequence encodes N |
| c 574 | 21 | 1.4 | 3006 | 10 | AAN91049 | Sequence encoding |
| c 575 | 21 | 1.4 | 3006 | 11 | AAQ05085 | Sequence encodes N |
| c 576 | 21 | 1.4 | 3012 | 24 | AAS96062 | Leishmania antigen |
| c 577 | 21 | 1.4 | 3092 | 24 | ABK14884 | DNA for APP-LacI f |
| c 578 | 21 | 1.4 | 3148 | 24 | AAL47324 | Amyloid precursor |
| c 579 | 21 | 1.4 | 3148 | 24 | ABK13303 | DNA encoding amylo |
| c 580 | 21 | 1.4 | 3238 | 23 | AAS83275 | DNA encoding novel |
| c 581 | 21 | 1.4 | 3243 | 19 | AAV32555 | Candida albicans C |
| c 582 | 21 | 1.4 | 3353 | 9 | AAN81234 | Sequence of human |
| c 583 | 21 | 1.4 | 3353 | 11 | AAQ04496 | Sequence of gene e |
| c 584 | 21 | 1.4 | 3353 | 12 | AAQ14097 | Amyloid precursor |
| c 585 | 21 | 1.4 | 3353 | 14 | AAQ54258 | Amyloid precursor |
| c 586 | 21 | 1.4 | 3353 | 21 | AAZ49951 | Human beta amyloid |
| c 587 | 21 | 1.4 | 3354 | 20 | AAZ32219 | Human beta amyloid |
| c 588 | 21 | 1.4 | 3354 | 21 | AAZ89477 | Human APP DNA. Ho |
| c 589 | 21 | 1.4 | 3414 | 23 | AAS83274 | DNA encoding novel |
| c 590 | 21 | 1.4 | 3520 | 20 | AAX77504 | Human beta-amyloid |
| c 591 | 21 | 1.4 | 3585 | 23 | AAS83273 | DNA encoding novel |
| c 592 | 21 | 1.4 | 3621 | 23 | ABV29298 | Human prostate exp |
| c 593 | 21 | 1.4 | 3648 | 23 | AAS83276 | DNA encoding novel |
| c 594 | 21 | 1.4 | 3742 | 23 | ABL23886 | Drosophila melanog |
| c 595 | 21 | 1.4 | 3910 | 21 | AAA30574 | Genomic DNA encodi |
| c 596 | 21 | 1.4 | 3910 | 24 | ABL55703 | Candida tropicalis |
| c 597 | 21 | 1.4 | 3910 | 24 | ABK31893 | Candida tropicalis |
| c 598 | 21 | 1.4 | 4122 | 23 | ABL28439 | Drosophila melanog |
| c 599 | 21 | 1.4 | 4231 | 23 | ABL13537 | Drosophila melanog |
| c 600 | 21 | 1.4 | 4287 | 23 | ABL27121 | Drosophila melanog |
| c 601 | 21 | 1.4 | 4844 | 23 | ABL09236 | Drosophila melanog |
| c 602 | 21 | 1.4 | 4929 | 24 | AAS96063 | Leishmania MAPS1A- |
| c 603 | 21 | 1.4 | 4958 | 24 | AAK98744 | Polynucleotide con |
| c 604 | 21 | 1.4 | 5293 | 24 | AAL44642 | Orphan intestinal |
| 605 | 21 | 1.4 | 5861 | 22 | AAK80814 | Human immune/haema |
| c 606 | 21 | 1.4 | 5950 | 23 | AAS72442 | DNA encoding novel |
| 607 | 21 | 1.4 | 6012 | 24 | ABK28338 | DNA transcription |
| 608 | 21 | 1.4 | 6607 | 22 | AAH98321 | Rabbit EST-derived |
| 609 | 21 | 1.4 | 6647 | 23 | ABL24638 | Drosophila melanog |
| 610 | 21 | 1.4 | 6655 | 22 | AAH99691 | Human protein enco |
| c 611 | 21 | 1.4 | 6708 | 23 | ABL28438 | Drosophila melanog |
| c 612 | 21 | 1.4 | 6868 | 22 | AAD16293 | Human APP-murine n |
| c 613 | 21 | 1.4 | 6916 | 21 | AAA28018 | Genomic DNA sequen |
| c 614 | 21 | 1.4 | 7137 | 24 | AAS95308 | Long terminal repe |
| 615 | 21 | 1.4 | 7876 | 23 | ABL13536 | Drosophila melanog |
| 616 | 21 | 1.4 | 8433 | 23 | ABL27120 | Drosophila melanog |
| c 617 | 21 | 1.4 | 8591 | 18 | AAT87083 | Plasmid pCLL602 en |
| c 618 | 21 | 1.4 | 8591 | 18 | AAT87084 | Plasmid pCLL621 en |
| c 619 | 21 | 1.4 | 8591 | 18 | AAT84561 | Plasmid pCLL602 en |
| c 620 | 21 | 1.4 | 8591 | 18 | AAT84562 | Plasmid pCLL621 en |
| c 621 | 21 | 1.4 | 8591 | 19 | AAV05849 | APP-REP 751 gene f |
| c 622 | 21 | 1.4 | 8591 | 19 | AAV05850 | APP-REP 751 gene f |
| c 623 | 21 | 1.4 | 8591 | 19 | AAV04865 | cDNA encoding amyl |
| c 624 | 21 | 1.4 | 8591 | 19 | AAV04866 | cDNA encoding amyl |
| 625 | 21 | 1.4 | 9434 | 23 | ABL17110 | Drosophila melanog |
| 626 | 21 | 1.4 | 11052 | 24 | ABK39985 | Human chemically p |
| 627 | 21 | 1.4 | 12537 | 17 | AAT41705 | Lymphocyte specifi |
| c 628 | 21 | 1.4 | 13023 | 23 | ABL03830 | Drosophila melanog |
| 629 | 21 | 1.4 | 15580 | 22 | ABA15958 | Human nervous syst |
| 630 | 21 | 1.4 | 17142 | 22 | AAS45497 | Chemically pretrea |
| 631 | 21 | 1.4 | 17142 | 24 | ABL34106 | Human immune syste |
| 632 | 21 | 1.4 | 17142 | 24 | ABK28429 | DNA transcription |
| c 633 | 21 | 1.4 | 17331 | 23 | ABL06072 | Drosophila melanog |
| 634 | 21 | 1.4 | 18028 | 23 | ABL13284 | Drosophila melanog |
| 635 | 21 | 1.4 | 22467 | 22 | AAS33423 | DNA encoding human |
| c 636 | 21 | 1.4 | 22467 | 22 | AAS33425 | DNA encoding human |
| 637 | 21 | 1.4 | 32082 | 22 | AAL06991 | Human reproductive |
| 638 | 21 | 1.4 | 47090 | 22 | AAK68725 | Human immune/haema |
| 639 | 21 | 1.4 | 47090 | 22 | AAK78219 | Human immune/haema |
| 640 | 21 | 1.4 | 62944 | 24 | ABL66947 | Lung cancer relate |
| 641 | 21 | 1.4 | 62944 | 24 | ABL68262 | Kidney cancer rela |
| c 642 | 21 | 1.4 | 145831 | 24 | ABL62309 | Colon adenocarcino |
| c 643 | 21 | 1.4 | 145831 | 24 | ABL66806 | Lung cancer relate |
| c 644 | 21 | 1.4 | 145831 | 24 | ABL68588 | Kidney cancer rela |
| c 645 | 21 | 1.4 | 145831 | 24 | ABL69213 | Prostate cancer re |
| c 646 | 21 | 1.4 | 167343 | 24 | ABL64403 | Stomach cancer rel |
| c 647 | 21 | 1.4 | 167343 | 24 | ABL67239 | Thyroid cancer rel |
| 648 | 21 | 1.4 | 215980 | 24 | AAL38337 | Complementary stra |
| 649 | 20 | 1.3 | 20 | 18 | AAT63597 | CD55 PCR primer us |
| c 650 | 20 | 1.3 | 20 | 18 | AAT63598 | CD55 PCR primer us |
| c 651 | 20 | 1.3 | 26 | 9 | AAN82052 | Probe O-CCA-26 for |
| 652 | 20 | 1.3 | 29 | 21 | AAC63576 | Guanosine rich oli |
| c 653 | 20 | 1.3 | 30 | 20 | AAX87920 | Human tumour assoc |
| 654 | 20 | 1.3 | 34 | 16 | AAQ99115 | cCIP DC oligo 54 - |
| 655 | 20 | 1.3 | 36 | 21 | AAZ46985 | Oligonucleotide us |
| c 656 | 20 | 1.3 | 38 | 17 | AAT06967 | Primer for microsa |
| c 657 | 20 | 1.3 | 42 | 17 | AAT31266 | Linker oligonucleo |
| c 658 | 20 | 1.3 | 42 | 18 | AAT79503 | NGF receptor p75-h |
| c 659 | 20 | 1.3 | 42 | 22 | AAH43439 | Primer J NS2 (919) |
| c 660 | 20 | 1.3 | 44 | 21 | AAZ46984 | Oligonucleotide us |
| 661 | 20 | 1.3 | 45 | 19 | AAV39026 | GnT-IV cDNA contai |
| 662 | 20 | 1.3 | 46 | 22 | AAF83288 | Human Chk1 DNA amp |
| c 663 | 20 | 1.3 | 48 | 24 | AAS16547 | Ligation independe |
| 664 | 20 | 1.3 | 51 | 19 | AAV55810 | Chimeric construct |
| c 665 | 20 | 1.3 | 52 | 17 | AAT46068 | Heparin binding pe |
| 666 | 20 | 1.3 | 52 | 24 | AAS16548 | Ligation independe |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 667 | 20 | 1.3 | 53 | 19 | AAV29093 | TBV25-Pfs28C fusio |
| c | 668 | 20 | 1.3 | 53 | 21 | AAA64666 | PCR primer used to |
| c | 669 | 20 | 1.3 | 54 | 24 | AAS16561 | Ligation independe |
| | 670 | 20 | 1.3 | 54 | 24 | AAS16562 | Ligation independe |
| c | 671 | 20 | 1.3 | 55 | 17 | AAT46074 | Fibronectin hepari |
| | 672 | 20 | 1.3 | 57 | 21 | AAA57194 | Human soluble subt |
| c | 673 | 20 | 1.3 | 58 | 17 | AAT46073 | Fibronectin hepari |
| c | 674 | 20 | 1.3 | 60 | 24 | ABL57146 | DNA encoding modif |
| | 675 | 20 | 1.3 | 65 | 24 | ABL40542 | Basidiomycetes man |
| c | 676 | 20 | 1.3 | 73 | 17 | AAT46066 | Heparin binding pe |
| | 677 | 20 | 1.3 | 74 | 21 | AAA87844 | Oligonucleotide RM |
| c | 678 | 20 | 1.3 | 76 | 18 | AAT90806 | Mouse persephin ge |
| c | 679 | 20 | 1.3 | 76 | 20 | AAX60475 | WO9914235 Seq ID N |
| | 680 | 20 | 1.3 | 80 | 21 | AAA87845 | Oligonucleotide RM |
| | 681 | 20 | 1.3 | 93 | 21 | AAA51731 | PTH functional dom |
| c | 682 | 20 | 1.3 | 103 | 17 | AAT46069 | TFPI heparin bindi |
| c | 683 | 20 | 1.3 | 126 | 22 | ABA73881 | Human foetal liver |
| c | 684 | 20 | 1.3 | 126 | 22 | AAK22333 | Human brain expres |
| c | 685 | 20 | 1.3 | 126 | 22 | AAK48499 | Human bone marrow |
| c | 686 | 20 | 1.3 | 126 | 22 | AAI54327 | Probe #23013 used |
| c | 687 | 20 | 1.3 | 130 | 21 | AAA31041 | Plant microsatelli |
| c | 688 | 20 | 1.3 | 147 | 21 | AAZ94527 | Cartilage-associat |
| | 689 | 20 | 1.3 | 158 | 22 | ABA46752 | Human breast cell |
| | 690 | 20 | 1.3 | 158 | 22 | ABA64632 | Human foetal liver |
| | 691 | 20 | 1.3 | 158 | 22 | ABA31759 | Probe #10225 for g |
| | 692 | 20 | 1.3 | 158 | 22 | AAK13070 | Human brain expres |
| | 693 | 20 | 1.3 | 158 | 22 | AAK38799 | Human bone marrow |
| | 694 | 20 | 1.3 | 158 | 22 | AAI19606 | Probe #9539 for ge |
| | 695 | 20 | 1.3 | 158 | 22 | AAI44802 | Probe #13488 used |
| | 696 | 20 | 1.3 | 158 | 22 | AAI05326 | Probe #5317 used t |
| | 697 | 20 | 1.3 | 158 | 24 | ABS12879 | Human genome-deriv |
| | 698 | 20 | 1.3 | 162 | 22 | ABA47258 | Human breast cell |
| | 699 | 20 | 1.3 | 162 | 22 | ABA65143 | Human foetal liver |
| | 700 | 20 | 1.3 | 162 | 22 | ABA75917 | Human foetal liver |
| | 701 | 20 | 1.3 | 162 | 22 | ABA32245 | Probe #10711 for g |
| | 702 | 20 | 1.3 | 162 | 22 | ABA40481 | Probe #18947 for g |
| | 703 | 20 | 1.3 | 162 | 22 | AAK13562 | Human brain expres |
| | 704 | 20 | 1.3 | 162 | 22 | AAK24598 | Human brain expres |
| | 705 | 20 | 1.3 | 162 | 22 | AAK39301 | Human bone marrow |
| | 706 | 20 | 1.3 | 162 | 22 | AAK50595 | Human bone marrow |
| | 707 | 20 | 1.3 | 162 | 22 | AAI20114 | Probe #10047 for g |
| | 708 | 20 | 1.3 | 162 | 22 | AAI27605 | Probe #17538 for g |
| | 709 | 20 | 1.3 | 162 | 22 | AAI45314 | Probe #14000 used |
| | 710 | 20 | 1.3 | 162 | 22 | AAI56574 | Probe #25260 used |
| | 711 | 20 | 1.3 | 162 | 22 | AAI05820 | Probe #5811 used t |
| | 712 | 20 | 1.3 | 162 | 24 | ABS13388 | Human genome-deriv |
| | 713 | 20 | 1.3 | 162 | 24 | ABS24067 | Human genome-deriv |
| c | 714 | 20 | 1.3 | 170 | 20 | AAZ27410 | K-ras plasmid temp |
| | 715 | 20 | 1.3 | 193 | 21 | AAZ94510 | Cartilage-associat |
| | 716 | 20 | 1.3 | 196 | 22 | ABA49704 | Human breast cell |
| | 717 | 20 | 1.3 | 196 | 22 | ABA67611 | Human foetal liver |
| | 718 | 20 | 1.3 | 196 | 22 | ABA34687 | Probe #13153 for g |
| | 719 | 20 | 1.3 | 196 | 22 | AAK16031 | Human brain expres |
| | 720 | 20 | 1.3 | 196 | 22 | AAK41777 | Human bone marrow |
| | 721 | 20 | 1.3 | 196 | 22 | AAI22534 | Probe #12467 for g |
| | 722 | 20 | 1.3 | 196 | 22 | AAI47827 | Probe #16513 used |
| | 723 | 20 | 1.3 | 196 | 22 | AAI08217 | Probe #8208 used t |
| | 724 | 20 | 1.3 | 196 | 24 | ABS15789 | Human genome-deriv |
| | 725 | 20 | 1.3 | 200 | 19 | AAV86016 | 5'-extension of th |
| c | 726 | 20 | 1.3 | 209 | 24 | ABK49239 | pET24d+ plasmid mu |
| | 727 | 20 | 1.3 | 210 | 21 | AAZ94503 | Cartilage-associat |
| c | 728 | 20 | 1.3 | 210 | 21 | AAA31045 | Plant microsatelli |
| | 729 | 20 | 1.3 | 221 | 22 | ABA47697 | Human breast cell |
| | 730 | 20 | 1.3 | 221 | 22 | ABA65591 | Human foetal liver |
| | 731 | 20 | 1.3 | 221 | 22 | ABA32679 | Probe #11145 for g |
| | 732 | 20 | 1.3 | 221 | 22 | AAK13994 | Human brain expres |
| | 733 | 20 | 1.3 | 221 | 22 | AAK39742 | Human bone marrow |
| | 734 | 20 | 1.3 | 221 | 22 | AAI20548 | Probe #10481 for g |
| | 735 | 20 | 1.3 | 221 | 22 | AAI45758 | Probe #14444 used |
| | 736 | 20 | 1.3 | 221 | 22 | AAI06247 | Probe #6238 used t |
| | 737 | 20 | 1.3 | 221 | 24 | ABS13836 | Human genome-deriv |
| | 738 | 20 | 1.3 | 226 | 22 | AAH35354 | Human colon cancer |
| | 739 | 20 | 1.3 | 241 | 20 | AAX87712 | Mouse sodium chann |
| | 740 | 20 | 1.3 | 242 | 22 | AAF30127 | Mouse sodium chann |
| | 741 | 20 | 1.3 | 245 | 21 | AAZ94508 | Cartilage-associat |
| | 742 | 20 | 1.3 | 249 | 22 | ABA46522 | Human breast cell |
| | 743 | 20 | 1.3 | 249 | 22 | ABA64381 | Human foetal liver |
| | 744 | 20 | 1.3 | 249 | 22 | ABA31526 | Probe #9992 for ge |
| | 745 | 20 | 1.3 | 249 | 22 | AAK12842 | Human brain expres |
| | 746 | 20 | 1.3 | 249 | 22 | AAK38570 | Human bone marrow |
| | 747 | 20 | 1.3 | 249 | 22 | AAI19369 | Probe #9302 for ge |
| | 748 | 20 | 1.3 | 249 | 22 | AAI44559 | Probe #13245 used |
| | 749 | 20 | 1.3 | 249 | 22 | AAI05096 | Probe #5087 used t |
| | 750 | 20 | 1.3 | 249 | 24 | ABS12635 | Human genome-deriv |
| | 751 | 20 | 1.3 | 252 | 16 | AAQ95202 | Simple tandem repe |
| | 752 | 20 | 1.3 | 277 | 21 | AAA31979 | Plant microsatelli |
| c | 753 | 20 | 1.3 | 279 | 21 | AAA80682 | Human secreted pro |
| c | 754 | 20 | 1.3 | 301 | 22 | AAI67267 | Mammaglobin polype |
| c | 755 | 20 | 1.3 | 302 | 21 | AAA31780 | Plant microsatelli |
| | 756 | 20 | 1.3 | 347 | 21 | AAA31712 | Plant microsatelli |
| | 757 | 20 | 1.3 | 354 | 24 | ABQ54132 | Human ovarian anti |
| c | 758 | 20 | 1.3 | 358 | 24 | ABQ85715 | Arabidopsis thalia |
| c | 759 | 20 | 1.3 | 367 | 21 | AAA31223 | Plant microsatelli |
| c | 760 | 20 | 1.3 | 370 | 22 | AAI83169 | Human polynucleoti |
| c | 761 | 20 | 1.3 | 374 | 22 | AAF66719 | Novel human polynu |
| | 762 | 20 | 1.3 | 375 | 21 | AAA31899 | Plant microsatelli |
| c | 763 | 20 | 1.3 | 381 | 21 | AAC56567 | Eucalyptus grandis |
| | 764 | 20 | 1.3 | 387 | 22 | ABA26070 | Probe #4536 for ge |
| c | 765 | 20 | 1.3 | 396 | 21 | AAA31104 | Plant microsatelli |
| c | 766 | 20 | 1.3 | 400 | 22 | AAS37355 | Novel human diagno |
| | 767 | 20 | 1.3 | 401 | 22 | ABA45299 | Human breast cell |
| | 768 | 20 | 1.3 | 401 | 22 | ABA55787 | Human foetal liver |
| | 769 | 20 | 1.3 | 401 | 22 | ABA25470 | Probe #3936 for ge |
| | 770 | 20 | 1.3 | 401 | 22 | AAK04010 | Human brain expres |
| | 771 | 20 | 1.3 | 401 | 22 | AAK29492 | Human bone marrow |
| | 772 | 20 | 1.3 | 401 | 22 | AAI14063 | Probe #3996 for ge |
| | 773 | 20 | 1.3 | 401 | 22 | AAI35443 | Probe #4129 used t |
| | 774 | 20 | 1.3 | 401 | 22 | AAI03921 | Probe #3912 used t |
| | 775 | 20 | 1.3 | 401 | 24 | ABS04041 | Human genome-deriv |
| c | 776 | 20 | 1.3 | 402 | 24 | ABN23907 | Human ORFX polynuc |
| | 777 | 20 | 1.3 | 405 | 24 | ABN16614 | Human ORFX polynuc |
| c | 778 | 20 | 1.3 | 414 | 23 | AAS74700 | DNA encoding novel |
| c | 779 | 20 | 1.3 | 417 | 22 | AAI82426 | Human polynucleoti |
| | 780 | 20 | 1.3 | 428 | 22 | ABA58052 | Human foetal liver |
| | 781 | 20 | 1.3 | 428 | 22 | ABA27301 | Probe #5767 for ge |
| | 782 | 20 | 1.3 | 428 | 22 | AAK06124 | Human brain expres |
| | 783 | 20 | 1.3 | 428 | 22 | AAK31777 | Human bone marrow |
| | 784 | 20 | 1.3 | 428 | 22 | AAI15823 | Probe #5756 for ge |
| | 785 | 20 | 1.3 | 428 | 22 | AAI37652 | Probe #6338 used t |
| | 786 | 20 | 1.3 | 428 | 24 | ABS06535 | Human genome-deriv |
| | 787 | 20 | 1.3 | 435 | 23 | ABL22911 | Drosophila melanog |
| | 788 | 20 | 1.3 | 438 | 21 | AAA31882 | Plant microsatelli |
| c | 789 | 20 | 1.3 | 440 | 21 | AAA31156 | Plant microsatelli |
| | 790 | 20 | 1.3 | 446 | 22 | ABA50433 | Human breast cell |
| | 791 | 20 | 1.3 | 446 | 22 | ABA68382 | Human foetal liver |
| | 792 | 20 | 1.3 | 446 | 22 | ABA35379 | Probe #13845 for g |
| | 793 | 20 | 1.3 | 446 | 22 | AAK16757 | Human brain expres |
| | 794 | 20 | 1.3 | 446 | 22 | AAK42529 | Human bone marrow |
| | 795 | 20 | 1.3 | 446 | 22 | AAI23276 | Probe #13209 for g |
| | 796 | 20 | 1.3 | 446 | 22 | AAI48596 | Probe #17282 used |
| | 797 | 20 | 1.3 | 446 | 22 | AAI08921 | Probe #8912 used t |
| | 798 | 20 | 1.3 | 446 | 24 | ABS16574 | Human genome-deriv |
| c | 799 | 20 | 1.3 | 461 | 19 | AAV29370 | Calcium ion channe |
| | 800 | 20 | 1.3 | 461 | 22 | ABA51975 | Human foetal liver |
| | 801 | 20 | 1.3 | 461 | 22 | ABA21793 | Probe #259 for gen |
| | 802 | 20 | 1.3 | 461 | 22 | AAK00261 | Human brain expres |
| | 803 | 20 | 1.3 | 461 | 22 | AAK25702 | Human bone marrow |
| | 804 | 20 | 1.3 | 461 | 22 | AAI10330 | Probe #263 for gen |
| | 805 | 20 | 1.3 | 461 | 22 | AAI31583 | Probe #269 used to |
| | 806 | 20 | 1.3 | 461 | 22 | AAI00266 | Probe #257 used to |
| | 807 | 20 | 1.3 | 461 | 24 | ABS00281 | Human genome-deriv |
| c | 808 | 20 | 1.3 | 464 | 24 | AAS61489 | Lung small cell ca |
| c | 809 | 20 | 1.3 | 465 | 21 | AAA31338 | Plant microsatelli |
| | 810 | 20 | 1.3 | 467 | 22 | ABA42568 | Human breast cell |
| | 811 | 20 | 1.3 | 467 | 22 | ABA52997 | Human foetal liver |
| | 812 | 20 | 1.3 | 467 | 22 | ABA22772 | Probe #1238 for ge |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 813 | 20 | 1.3 | 467 | 22 | AAK01245 | Human brain expres |
| | 814 | 20 | 1.3 | 467 | 22 | AAK26707 | Human bone marrow |
| | 815 | 20 | 1.3 | 467 | 22 | AAI11333 | Probe #1266 for ge |
| | 816 | 20 | 1.3 | 467 | 22 | AAI32602 | Probe #1288 used t |
| | 817 | 20 | 1.3 | 467 | 22 | AAI01249 | Probe #1240 used t |
| | 818 | 20 | 1.3 | 467 | 24 | ABS01301 | Human genome-deriv |
| | 819 | 20 | 1.3 | 476 | 22 | ABA51702 | Human foetal liver |
| | 820 | 20 | 1.3 | 476 | 22 | ABA21540 | Probe #6 for gene |
| | 821 | 20 | 1.3 | 476 | 22 | AAK00015 | Human brain expres |
| | 822 | 20 | 1.3 | 476 | 22 | AAK25450 | Human bone marrow |
| | 823 | 20 | 1.3 | 476 | 22 | AAI10073 | Probe #6 for gene |
| | 824 | 20 | 1.3 | 476 | 22 | AAI31321 | Probe #7 used to m |
| | 825 | 20 | 1.3 | 476 | 22 | AAI00016 | Probe #7 used to m |
| | 826 | 20 | 1.3 | 476 | 24 | ABS00015 | Human genome-deriv |
| | 827 | 20 | 1.3 | 481 | 21 | AAA27455 | Argemone mexicana |
| c | 828 | 20 | 1.3 | 484 | 22 | ABA43815 | Human breast cell |
| c | 829 | 20 | 1.3 | 484 | 22 | ABA54270 | Human foetal liver |
| c | 830 | 20 | 1.3 | 484 | 22 | ABA24025 | Probe #2491 for ge |
| c | 831 | 20 | 1.3 | 484 | 22 | AAK02548 | Human brain expres |
| c | 832 | 20 | 1.3 | 484 | 22 | AAK27987 | Human bone marrow |
| c | 833 | 20 | 1.3 | 484 | 22 | AAI12569 | Probe #2502 for ge |
| c | 834 | 20 | 1.3 | 484 | 22 | AAI33916 | Probe #2602 used t |
| c | 835 | 20 | 1.3 | 484 | 22 | AAI02476 | Probe #2467 used t |
| c | 836 | 20 | 1.3 | 484 | 24 | ABS02453 | Human genome-deriv |
| c | 837 | 20 | 1.3 | 491 | 21 | AAC79301 | Human lung tumour- |
| | 838 | 20 | 1.3 | 491 | 22 | ABA42104 | Human breast cell |
| | 839 | 20 | 1.3 | 491 | 22 | ABA52526 | Human foetal liver |
| | 840 | 20 | 1.3 | 491 | 22 | ABA22315 | Probe #781 for gen |
| | 841 | 20 | 1.3 | 491 | 22 | AAK00790 | Human brain expres |
| | 842 | 20 | 1.3 | 491 | 22 | AAK26242 | Human bone marrow |
| | 843 | 20 | 1.3 | 491 | 22 | AAI10875 | Probe #808 for gen |
| | 844 | 20 | 1.3 | 491 | 22 | AAI32135 | Probe #821 used to |
| | 845 | 20 | 1.3 | 491 | 22 | AAI00799 | Probe #790 used to |
| c | 846 | 20 | 1.3 | 491 | 23 | AAD23377 | Human lung tumour- |
| | 847 | 20 | 1.3 | 491 | 24 | ABS00830 | Human genome-deriv |
| c | 848 | 20 | 1.3 | 492 | 23 | ABL04957 | Drosophila melanog |
| c | 849 | 20 | 1.3 | 509 | 20 | AAV89057 | EST clone CB239. |
| c | 850 | 20 | 1.3 | 512 | 23 | AAS74335 | DNA encoding novel |
| | 851 | 20 | 1.3 | 520 | 24 | ABQ33760 | Oligonucleotide fo |
| c | 852 | 20 | 1.3 | 520 | 24 | ABQ33761 | Oligonucleotide fo |
| c | 853 | 20 | 1.3 | 530 | 21 | AAA95215 | Human OCT-T1 parti |
| | 854 | 20 | 1.3 | 534 | 20 | AAV86789 | EST clone BF263. |
| c | 855 | 20 | 1.3 | 544 | 22 | ABA61382 | Human foetal liver |
| c | 856 | 20 | 1.3 | 544 | 22 | AAK09681 | Human brain expres |
| c | 857 | 20 | 1.3 | 544 | 22 | AAK35573 | Human bone marrow |
| c | 858 | 20 | 1.3 | 544 | 22 | AAI41288 | Probe #9974 used t |
| | 859 | 20 | 1.3 | 560 | 22 | AAK92562 | Human cDNA 3'-end |
| | 860 | 20 | 1.3 | 573 | 22 | ABA15777 | Human nervous syst |
| | 861 | 20 | 1.3 | 586 | 22 | ABA63563 | Human foetal liver |
| | 862 | 20 | 1.3 | 586 | 22 | ABA30758 | Probe #9224 for ge |
| | 863 | 20 | 1.3 | 586 | 22 | AAK12090 | Human brain expres |
| | 864 | 20 | 1.3 | 586 | 22 | AAK37806 | Human bone marrow |
| | 865 | 20 | 1.3 | 586 | 22 | AAI18562 | Probe #8495 for ge |
| | 866 | 20 | 1.3 | 586 | 22 | AAI43676 | Probe #12362 used |
| | 867 | 20 | 1.3 | 586 | 24 | ABS11798 | Human genome-deriv |
| c | 868 | 20 | 1.3 | 612 | 23 | ABL27195 | Drosophila melanog |
| c | 869 | 20 | 1.3 | 621 | 23 | ABL28471 | Drosophila melanog |
| c | 870 | 20 | 1.3 | 623 | 21 | AAZ47117 | Rice Act1-GUS fusi |
| c | 871 | 20 | 1.3 | 623 | 24 | ABK86738 | Rice Act1 gene. O |
| c | 872 | 20 | 1.3 | 666 | 23 | AAS72572 | DNA encoding novel |
| c | 873 | 20 | 1.3 | 720 | 23 | ABL26987 | Drosophila melanog |
| c | 874 | 20 | 1.3 | 723 | 21 | AAC57290 | Eucalyptus grandis |
| c | 875 | 20 | 1.3 | 797 | 24 | ABK34450 | Human cDNA for nov |
| | 876 | 20 | 1.3 | 858 | 15 | AAQ55451 | Pgs28 protein codi |
| | 877 | 20 | 1.3 | 858 | 16 | AAQ87432 | P. gallinaceum Pgs |
| | 878 | 20 | 1.3 | 890 | 24 | ABQ34484 | Oligonucleotide fo |
| c | 879 | 20 | 1.3 | 890 | 24 | ABQ34485 | Oligonucleotide fo |
| | 880 | 20 | 1.3 | 905 | 21 | AAA27457 | Veronia mespilifol |
| | 881 | 20 | 1.3 | 906 | 23 | AAS87198 | DNA encoding novel |
| c | 882 | 20 | 1.3 | 906 | 23 | AAS91420 | DNA encoding novel |
| c | 883 | 20 | 1.3 | 930 | 20 | AAZ20102 | Soybean serine pal |
| c | 884 | 20 | 1.3 | 940 | 23 | ABL02141 | Drosophila melanog |
| c | 885 | 20 | 1.3 | 941 | 16 | AAT03745 | Human gax gene. H |
| c | 886 | 20 | 1.3 | 942 | 21 | AAC69411 | Human secreted pro |
| c | 887 | 20 | 1.3 | 942 | 21 | AAA27456 | Soybean LEC1 # 1 c |
| c | 888 | 20 | 1.3 | 945 | 23 | ABL21661 | Drosophila melanog |
| c | 889 | 20 | 1.3 | 947 | 24 | ABK17112 | Eucalyptus grandis |
| | 890 | 20 | 1.3 | 968 | 22 | ABA63990 | Human foetal liver |
| | 891 | 20 | 1.3 | 968 | 22 | ABA31163 | Probe #9629 for ge |
| | 892 | 20 | 1.3 | 968 | 22 | AAK12490 | Human brain expres |
| | 893 | 20 | 1.3 | 968 | 22 | AAK38199 | Human bone marrow |
| | 894 | 20 | 1.3 | 968 | 22 | AAI18991 | Probe #8924 for ge |
| | 895 | 20 | 1.3 | 968 | 22 | AAI44129 | Probe #12815 used |
| | 896 | 20 | 1.3 | 968 | 24 | ABS12234 | Human genome-deriv |
| | 897 | 20 | 1.3 | 971 | 23 | ABL04343 | Drosophila melanog |
| c | 898 | 20 | 1.3 | 972 | 23 | ABL25303 | Drosophila melanog |
| c | 899 | 20 | 1.3 | 1008 | 20 | AAX16158 | Human HoxA1 varian |
| c | 900 | 20 | 1.3 | 1008 | 20 | AAX16155 | Human wild-type Ho |
| c | 901 | 20 | 1.3 | 1026 | 21 | AAC47690 | Arabidopsis thalia |
| c | 902 | 20 | 1.3 | 1041 | 21 | AAA62731 | Endoglucanase nucl |
| c | 903 | 20 | 1.3 | 1041 | 24 | AAL43249 | Phycomyces nitens |
| c | 904 | 20 | 1.3 | 1051 | 23 | ABL14157 | Drosophila melanog |
| c | 905 | 20 | 1.3 | 1053 | 23 | AAS77066 | DNA encoding novel |
| | 906 | 20 | 1.3 | 1060 | 20 | AAV71740 | Rice OsMADS7 cDNA. |
| | 907 | 20 | 1.3 | 1060 | 21 | AAL44854 | Plant flowering ti |
| | 908 | 20 | 1.3 | 1072 | 24 | ABQ43832 | Oligonucleotide fo |
| c | 909 | 20 | 1.3 | 1072 | 24 | ABQ43833 | Oligonucleotide fo |
| | 910 | 20 | 1.3 | 1075 | 22 | ABA48937 | Human breast cell |
| | 911 | 20 | 1.3 | 1075 | 22 | ABA66852 | Human foetal liver |
| | 912 | 20 | 1.3 | 1075 | 22 | ABA33921 | Probe #12387 for g |
| | 913 | 20 | 1.3 | 1075 | 22 | AAK15288 | Human brain expres |
| | 914 | 20 | 1.3 | 1075 | 22 | AAK41011 | Human bone marrow |
| | 915 | 20 | 1.3 | 1075 | 22 | AAI21781 | Probe #11714 for g |
| | 916 | 20 | 1.3 | 1075 | 22 | AAI47064 | Probe #15750 used |
| | 917 | 20 | 1.3 | 1075 | 22 | AAI07466 | Probe #7457 used t |
| | 918 | 20 | 1.3 | 1075 | 24 | ABS14983 | Human genome-deriv |
| | 919 | 20 | 1.3 | 1100 | 21 | AAC37083 | Arabidopsis thalia |
| | 920 | 20 | 1.3 | 1108 | 21 | AAC51559 | Arabidopsis thalia |
| | 921 | 20 | 1.3 | 1152 | 21 | AAC39862 | Arabidopsis thalia |
| c | 922 | 20 | 1.3 | 1160 | 21 | AAC39976 | Arabidopsis thalia |
| c | 923 | 20 | 1.3 | 1163 | 23 | ABL21205 | Drosophila melanog |
| c | 924 | 20 | 1.3 | 1174 | 22 | AAS44729 | Dog full-length po |
| | 925 | 20 | 1.3 | 1199 | 21 | AAC50442 | Arabidopsis thalia |
| | 926 | 20 | 1.3 | 1200 | 21 | AAC39052 | Arabidopsis thalia |
| c | 927 | 20 | 1.3 | 1203 | 20 | AAZ00869 | Human c-Maf cDNA. |
| c | 928 | 20 | 1.3 | 1205 | 22 | AAC85551 | cDNA encoding CDIF |
| c | 929 | 20 | 1.3 | 1215 | 22 | AAK79063 | Human immune/haema |
| c | 930 | 20 | 1.3 | 1251 | 24 | ABK09969 | Eastern cottonmout |
| c | 931 | 20 | 1.3 | 1266 | 20 | AAX09011 | Brn-3a polynucleot |
| c | 932 | 20 | 1.3 | 1266 | 21 | AAA29007 | Murine transcripti |
| c | 933 | 20 | 1.3 | 1272 | 20 | AAX09010 | Brn-3a polynucleot |
| c | 934 | 20 | 1.3 | 1272 | 21 | AAA29006 | Human transcriptio |
| c | 935 | 20 | 1.3 | 1305 | 22 | AAC84644 | ProtL-CBDcex encod |
| c | 936 | 20 | 1.3 | 1305 | 22 | AAF24725 | Nucleotide sequenc |
| c | 937 | 20 | 1.3 | 1307 | 21 | AAA63927 | DNA encoding prote |
| c | 938 | 20 | 1.3 | 1330 | 21 | AAC47157 | Arabidopsis thalia |
| c | 939 | 20 | 1.3 | 1335 | 23 | ABL28561 | Drosophila melanog |
| c | 940 | 20 | 1.3 | 1337 | 12 | AAQ13880 | Cellular DNA-bindi |
| c | 941 | 20 | 1.3 | 1347 | 23 | AAS72571 | DNA encoding novel |
| c | 942 | 20 | 1.3 | 1365 | 23 | ABL17751 | Drosophila melanog |
| | 943 | 20 | 1.3 | 1371 | 21 | AAC44690 | Arabidopsis thalia |
| c | 944 | 20 | 1.3 | 1380 | 23 | ABL16541 | Drosophila melanog |
| c | 945 | 20 | 1.3 | 1392 | 18 | AAT80053 | Rice actin 1 gene |
| c | 946 | 20 | 1.3 | 1392 | 24 | ABK64832 | Human benign prost |
| c | 947 | 20 | 1.3 | 1395 | 23 | AAS89524 | DNA encoding novel |
| c | 948 | 20 | 1.3 | 1398 | 21 | AAC49466 | Arabidopsis thalia |
| | 949 | 20 | 1.3 | 1403 | 22 | ABA43834 | Human breast cell |
| | 950 | 20 | 1.3 | 1403 | 22 | ABA54290 | Human foetal liver |
| | 951 | 20 | 1.3 | 1403 | 22 | ABA24047 | Probe #2513 for ge |
| | 952 | 20 | 1.3 | 1403 | 22 | AAK02574 | Human brain expres |
| | 953 | 20 | 1.3 | 1403 | 22 | AAK28010 | Human bone marrow |
| | 954 | 20 | 1.3 | 1403 | 22 | AAI12593 | Probe #2526 for ge |
| | 955 | 20 | 1.3 | 1403 | 22 | AAI33941 | Probe #2627 used t |
| | 956 | 20 | 1.3 | 1403 | 22 | AAI02498 | Probe #2489 used t |
| | 957 | 20 | 1.3 | 1403 | 24 | ABS02482 | Human genome-deriv |
| c | 958 | 20 | 1.3 | 1428 | 22 | AAI89339 | Human polynucleoti |

| | | | | | | |
|---|---|---|---|---|---|---|
| c 959 | 20 | 1.3 | 1440 | 23 | AAS87699 | DNA encoding novel |
| 960 | 20 | 1.3 | 1440 | 23 | AAS87786 | DNA encoding novel |
| c 961 | 20 | 1.3 | 1452 | 20 | AAZ00461 | Human secreted pro |
| c 962 | 20 | 1.3 | 1463 | 23 | AAS82804 | DNA encoding novel |
| c 963 | 20 | 1.3 | 1512 | 23 | ABL22001 | Drosophila melanog |
| c 964 | 20 | 1.3 | 1521 | 19 | AAV42338 | DNA encoding trypa |
| 965 | 20 | 1.3 | 1561 | 19 | AAV27384 | Streptococcus pneu |
| 966 | 20 | 1.3 | 1561 | 23 | ABL10289 | Drosophila melanog |
| 967 | 20 | 1.3 | 1561 | 24 | ABQ84852 | S. pneumoniae SP07 |
| c 968 | 20 | 1.3 | 1563 | 22 | AAS44728 | Human full-length |
| c 969 | 20 | 1.3 | 1568 | 24 | ABK64525 | Human benign prost |
| c 970 | 20 | 1.3 | 1590 | 23 | AAS69779 | DNA encoding novel |
| c 971 | 20 | 1.3 | 1594 | 23 | AAS75944 | DNA encoding novel |
| 972 | 20 | 1.3 | 1599 | 19 | AAV86017 | Mouse Lrp5 cDNA op |
| 973 | 20 | 1.3 | 1602 | 21 | AAC41493 | Arabidopsis thalia |
| c 974 | 20 | 1.3 | 1602 | 22 | AAD11112 | Human small cell l |
| c 975 | 20 | 1.3 | 1602 | 24 | AAS61863 | Lung small cell ca |
| 976 | 20 | 1.3 | 1614 | 21 | AAC45832 | Arabidopsis thalia |
| c 977 | 20 | 1.3 | 1635 | 22 | ABA49946 | Human breast cell |
| c 978 | 20 | 1.3 | 1635 | 22 | ABA67865 | Human foetal liver |
| c 979 | 20 | 1.3 | 1635 | 22 | ABA34921 | Probe #13387 for g |
| c 980 | 20 | 1.3 | 1635 | 22 | AAK16270 | Human brain expres |
| c 981 | 20 | 1.3 | 1635 | 22 | AAK42016 | Human bone marrow |
| c 982 | 20 | 1.3 | 1635 | 22 | AAI22780 | Probe #12713 for g |
| c 983 | 20 | 1.3 | 1635 | 22 | AAI48082 | Probe #16768 used |
| c 984 | 20 | 1.3 | 1635 | 22 | AAI08454 | Probe #8445 used t |
| c 985 | 20 | 1.3 | 1635 | 24 | ABS16047 | Human genome-deriv |
| c 986 | 20 | 1.3 | 1647 | 22 | AAH33982 | Human colon cancer |
| c 987 | 20 | 1.3 | 1655 | 21 | AAZ61589 | DNA encoding a hum |
| c 988 | 20 | 1.3 | 1655 | 21 | AAZ61592 | DNA encoding a hum |
| 989 | 20 | 1.3 | 1680 | 23 | AAS85388 | DNA encoding novel |
| c 990 | 20 | 1.3 | 1686 | 23 | AAS74389 | DNA encoding novel |
| c 991 | 20 | 1.3 | 1692 | 20 | AAX87663 | HGF-MSP hybrid pro |
| 992 | 20 | 1.3 | 1711 | 19 | AAV86015 | Mouse Lrp5 cDNA po |
| c 993 | 20 | 1.3 | 1725 | 20 | AAX87662 | Hepatocyte growth |
| c 994 | 20 | 1.3 | 1773 | 23 | AAS87202 | DNA encoding novel |
| c 995 | 20 | 1.3 | 1785 | 22 | ABA19406 | Human nervous syst |
| c 996 | 20 | 1.3 | 1785 | 23 | ABL09091 | Drosophila melanog |
| c 997 | 20 | 1.3 | 1803 | 21 | AAA97202 | A. thaliana NIM1 h |
| 998 | 20 | 1.3 | 1812 | 22 | AAI86813 | Human polynucleoti |
| c 999 | 20 | 1.3 | 1817 | 24 | ABK34945 | Human cDNA encodin |
| c1000 | 20 | 1.3 | 1818 | 21 | AAA97233 | A. thaliana NIM1 h |

ALIGNMENTS

```
RESULT 1
AAX87915
ID   AAX87915 standard; cDNA; 1493 BP.
XX
AC   AAX87915;
XX
DT   22-NOV-1999  (first entry)
XX
DE   Human tumour associated antigen 791Tgp72 cDNA.
XX
KW   791Tgp72; tumour associated antigen; CD55; colorectal cancer;
KW   breast cancer; ovary cancer; osteosarcoma; vaccine; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             199..1344
FT                   /*tag=  a
XX
PN   WO9943800-A1.
XX
PD   02-SEP-1999.
XX
PF   26-FEB-1999;   99WO-GB00582.
XX
PR   26-FEB-1998;   98GB-0004065.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Durrant LG,  Spendlove I;
XX
DR   WPI; 1999-540585/45.
DR   P-PSDB; AAY31740.
XX
PT   Cancer vaccine containing CD55 family polypeptide, to induce at
PT   least one of T helper, cytotoxic T cell or natural killer immune
PT   response
XX
PS   Claim 14; Fig 11; P 82pp; English.
XX
CC   This is the nucleotide sequence of cDNA coding for human 791Tgp72
CC   (see AAY31740), a new member of the CD55 family that is over-expressed
CC   on a wide range of solid tumours.  The cDNA was isolated from
CC   osteosarcoma cell line 791T cell cDNA by PCR amplification using
CC   primers (see AAX87916-22) based on an isolated N-terminal peptide of
CC   791Tgp72.  A claimed cancer vaccine comprises a polypeptide of the
CC   CD55 family, including full-length CD55 or 791Tgp72, or an antigen,
CC   polypeptide, fragment or derivative of CD55 or 791Tgp72.  Claimed
CC   cancer vaccines also include nucleic acids encoding CD55 or 791Tgp72
CC   antigen, polypeptide, fragment or derivative.  Claimed methods of
CC   treating a cancer patient involve administering the cancer vaccine.
CC   CD55 and 791Tgp72 have identical amino acid sequences and are
CC   encoded by cDNA which is identical over the entire coding region,
CC   through differences exist in the 5' and 3' non-coding regions and
CC   in the glycosylation pattern of the proteins.  The cancer vaccines
CC   induce at least one of T helper, cytotoxic T cell or natural killer
CC   immune responses, possibly also production of neutralizing
CC   antibodies and complement-mediated lysis.  They are useful for
CC   treating e.g. colorectal, breast or ovarian cancer or osteosarcoma,
CC   where these are associated with overexpression of 791Tgp72.
XX
SQ   Sequence 1493 BP; 401 A; 355 C; 355 G; 382 T; 0 other;

  Query Match             100.0%;  Score 1493;  DB 20;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCTGCCCATCTTGTCGTCGTCGTCCTTGTA 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TTTAAACGGGCCCTCTAGACTCGAGCGGCCGCTGCCCATCTTGTCGTCGTCGTCCTTGTA 60

Qy      61 GTCGTGCATGTGGTGGTGGTGGTGGTGGTTAACCATGGTGGCGGGCCGCCACTGTGCTGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GTCGTGCATGTGGTGGTGGTGGTGGTGGTTAACCATGGTGGCGGGCCGCCACTGTGCTGG 120

Qy     121 ATATCTGCAGAATTCGATGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTT 180
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Qy     181 GTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTC 240
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Db     181 GTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTC 240

Qy     241 CTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     301 GACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGT 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     361 TTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGC 420

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Db     421 GAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGC 480
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Qy    481 AATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATC 540
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Db    481 AATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATC 540

Qy    541 ACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGA 600
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Db    601 AGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCA 660

Qy    661 GTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATT 720
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Qy    721 GATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTAC 780
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Qy    781 AAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGT 840
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Qy    841 GACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGA 900
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Qy    901 ATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAAT 960
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Qy    961 AAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGA 1020
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Qy   1321 GTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTAT 1380
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RESULT 2
AAN70047
ID AAN70047 standard; cDNA; 2015 BP.
XX
AC AAN70047;
XX
DT 03-OCT-2002 (updated)
DT 03-FEB-1991 (first entry)
XX
DE Encodes human decay acceleration factor variant #1.
XX
KW Decay acceleration factor; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /label=mRNA splice site
FT mat_peptide 66..1210
FT /*tag= b
FT /product=decay acceleration factor variant
XX
PN EP244267-A.
XX
PD 04-NOV-1987.
XX
PF 01-MAY-1987; 87EP-0303944.
XX
PR 02-MAY-1986; 86US-0859107.
XX
PA (GETH ) GENENTECH INC.
XX
PI Caras IW;
XX
DR WPI; 1987-308481/44.
DR P-PSDB; AAP70048.
XX
PT New decay accelerating factor variants - obtained with the factor by
PT using recombinant DNA procedures.
XX
PS Disclosure; Page 15-17; 20pp; English.
XX
CC The cDNA sequence is that of clones phage lambda 33 (to the
CC HindIII site at residue 1) and phage lambda 47 (HindIII to
CC the 3' end) encoding a variant of DAF. DAF and variants are
CC useful for treating paraoxysmal nocturnal haemoglobinuria,
CC or inflammatory or cell lytic autoimmune diseases. They may
CC be used to ameliorate allograft rejection or autoimmune
CC diseases. See also AAN70046, AAN70048.
CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ Sequence 2015 BP; 639 A; 402 C; 427 G; 547 T; 0 other;

```
  Query Match             90.8%;  Score 1356;  DB 8;  Length 2015;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304
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Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||||||||||
Db   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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RESULT 3
AAX87914
ID   AAX87914 standard; cDNA; 2102 BP.
XX
AC   AAX87914;
XX
DT   22-NOV-1999  (first entry)
XX
DE   Human CD55 tumour associated antigen cDNA.
XX
KW   CD55; decay accelerating factor; DAF; tumour associated antigen;
KW   791Tgp72; colorectal cancer; breast cancer; ovary cancer;
KW   osteosarcoma; vaccine; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1211
FT                   /*tag= a
FT   sig_peptide     66..167
FT                   /*tag= b
FT   mat_peptide     168..1208
FT                   /*tag= c
XX
PN   WO9943800-A1.
XX
PD   02-SEP-1999.
XX
PF   26-FEB-1999;   99WO-GB00582.
XX
PR   26-FEB-1998;   98GB-0004065.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Durrant LG,  Spendlove I;
XX
DR   WPI; 1999-540585/45.
DR   P-PSDB; AAY31740.
XX
PT   Cancer vaccine containing CD55 family polypeptide, to induce at
PT   least one of T helper, cytotoxic T cell or natural killer immune
PT   response
XX
PS   Claim 14; Fig 10; P 82pp; English.
XX
CC   This is the nucleotide sequence of cDNA coding for human CD55 (see
CC   AAY31740) or decay accelerating factor (DAF), which is over-expressed
CC   on a wide range of solid tumours.  A claimed cancer vaccine
CC   comprises a polypeptide of the CD55 family, including full-length
CC   CD55 or the new tumour associated antigen 791Tgp72, or an antigen,
CC   polypeptide, fragment or derivative of CD55 or 791Tgp72.  Claimed
CC   cancer vaccines also include nucleic acids encoding CD55 or 791Tgp72
CC   antigen, polypeptide, fragment or derivative.  Claimed methods of
CC   treating a cancer patient involve administering the cancer vaccine.
CC   CD55 and 791Tgp72 have identical amino acid sequences and are
CC   encoded by cDNA which is identical over the entire coding region,
CC   through differences exist in the 5' and 3' non-coding regions and
CC   in the glycosylation pattern of the proteins.  The cancer vaccines
CC   induce at least one of T helper, cytotoxic T cell or natural killer
CC   immune responses, possibly also production of neutralizing
CC   antibodies and complement-mediated lysis.  They are useful for
CC   treating e.g. colorectal, breast or ovarian cancer or osteosarcoma,
CC   where these are associated with overexpression of 791Tgp72.
XX
SQ   Sequence 2102 BP; 661 A; 419 C; 445 G; 577 T; 0 other;

  Query Match             90.8%;  Score 1356;  DB 20;  Length 2102;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy    1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy    1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy    1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy    1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
           |||||||||||||||||||||||||||||||||||
Db    1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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RESULT 4
ABK83991
ID  ABK83991 standard; cDNA; 2102 BP.
XX
AC  ABK83991;
XX
DT  14-AUG-2002  (first entry)
XX
DE  Human cDNA differentially expressed in granulocytic cells #562.
XX
KW  Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW  viral infection; parasitic infection; protozoal infection;
KW  fungal infection; sterile inflammatory disease; psoriasis;
KW  rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW  cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW  adult respiratory distress syndrome; inflammatory bowel disease;
KW  Crohn's disease; ulcerative colitis; periodontal disease;
KW  granulocyte activation; chronic inflammation; allergy.
XX
OS  Homo sapiens.
XX
PN  WO200228999-A2.
XX
PD  11-APR-2002.
XX
PF  03-OCT-2001; 2001WO-US30821.
XX
PR  03-OCT-2000; 2000US-237189P.
XX
PA  (GENE-) GENE LOGIC INC.
XX
PI  Beazer-Barclay Y,  Weissman SM,  Yamaga S,  Vockley J;
XX
DR  WPI; 2002-435328/46.
XX
PT  Detecting granulocyte activation by detecting differential expression
PT  of genes associated with granulocyte activation, which serves as
PT  diagnostic markers that is useful for monitoring disease states and
PT  drug toxicity  -
XX
PS  Claim 1; SEQ ID No 562; 114pp; English.
XX
CC  The invention relates to detecting (M1) granulocyte (GC) activation
CC  (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC  DNA chip analysis as given in the specification, and comparing
CC  the expression level to an expression level in an unactivated
CC  GC, where differential expression of Gs is indicative of GCA.
CC  Also included are modulating (M2) GA by contacting GC with an agent
CC  that alters the expression of at least one gene in Gs; (2) screening (M3)
CC  for an agent capable of modulating GCA or an inflammation (especially
CC  chronic) in a tissue, an allergic response in a subject, exposure of a
CC  subject to a pathogen or sterile inflammatory disease using the
CC  gene expression profile; (3) detecting (M4) an inflammation (especially
CC  chronic) in a tissue, an allergic response in a subject, exposure of a
CC  subject to a pathogen or sterile inflammatory disease, by detecting the

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CC   level of expression in a sample of the tissue of gene(s) from Gs, where
CC   the level of expression of the gene is indicative of inflammation;
CC   (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC   an allergic response in a subject, exposure of a subject to a pathogen
CC   or sterile inflammatory disease, by contacting a tissue having
CC   inflammation with an agent that modulates the expression of gene(s)
CC   from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC   modulating GA; M3 is useful for screening an agent capable of modulating
CC   GCA preferably in an inflammation in a tissue; M4 is useful for
CC   detecting an inflammation (especially chronic) in a tissue, an allergic
CC   response in a subject, exposure of a subject to a pathogen or sterile
CC   inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC   glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC   reperfusion injury, ARDS, adult respiratory distress syndrome,
CC   inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC   periodontal disease; also bacterial infection, viral infection,
CC   parasitic infection, protozoal infection, fungal infection and M5 is
CC   useful for treating one of the above conditions. The present
CC   sequence represents a gene differentially expressed in granulocytes.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2102 BP; 661 A; 419 C; 445 G; 577 T; 0 other;

  Query Match             90.8%;  Score 1356;  DB 24;  Length 2102;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy    1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
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Db    1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy    1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy    1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy    1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db    1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360


RESULT 5
ABL65229
ID   ABL65229 standard; DNA; 2102 BP.
XX
AC   ABL65229;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Lung cancer related gene sequence SEQ ID NO:3566.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US10838.
XX
```

PR 05-JUN-2000; 2000US-209473P.
PR 05-JUN-2000; 2000US-209531P.
PR 18-SEP-2000; 2000US-233133P.
PR 18-SEP-2000; 2000US-233617P.
PR 20-SEP-2000; 2000US-234009P.
PR 20-SEP-2000; 2000US-234034P.
PR 20-SEP-2000; 2000US-234052P.
PR 22-SEP-2000; 2000US-234509P.
PR 22-SEP-2000; 2000US-234567P.
PR 25-SEP-2000; 2000US-234923P.
PR 25-SEP-2000; 2000US-234924P.
PR 25-SEP-2000; 2000US-235077P.
PR 25-SEP-2000; 2000US-235082P.
PR 25-SEP-2000; 2000US-235134P.
PR 25-SEP-2000; 2000US-235280P.
PR 26-SEP-2000; 2000US-235637P.
PR 26-SEP-2000; 2000US-235638P.
PR 27-SEP-2000; 2000US-235711P.
PR 27-SEP-2000; 2000US-235720P.
PR 27-SEP-2000; 2000US-235840P.
PR 27-SEP-2000; 2000US-235863P.
PR 28-SEP-2000; 2000US-236028P.
PR 28-SEP-2000; 2000US-236032P.
PR 28-SEP-2000; 2000US-236033P.
PR 28-SEP-2000; 2000US-236034P.
PR 28-SEP-2000; 2000US-236109P.
PR 28-SEP-2000; 2000US-236111P.
PR 29-SEP-2000; 2000US-236842P.
PR 29-SEP-2000; 2000US-236891P.
PR 02-OCT-2000; 2000US-237172P.
PR 02-OCT-2000; 2000US-237173P.
PR 02-OCT-2000; 2000US-237278P.
PR 02-OCT-2000; 2000US-237294P.
PR 02-OCT-2000; 2000US-237295P.
PR 02-OCT-2000; 2000US-237316P.
PR 03-OCT-2000; 2000US-237425P.
PR 03-OCT-2000; 2000US-237598P.
PR 03-OCT-2000; 2000US-237604P.
PR 03-OCT-2000; 2000US-237606P.
PR 03-OCT-2000; 2000US-237608P.
PR 01-NOV-2000; 2000US-244867P.
PR 01-NOV-2000; 2000US-245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a
PT chemical agent to be tested for anti-neoplastic activity, and
PT determining a change in expression of a gene of a signature gene set -
XX
PS Claim 1; SEQ ID 3566; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an
CC anti-neoplastic agent. The method involves exposing cells to a chemical
CC agent to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening
CC an anti-neoplastic agent, and can be used for producing a product which
CC is the data collected with respect to the anti-neoplastic agent as a
CC result of M1, and the data is sufficient to convey the chemical
CC structure and/or properties of the agent. M1 can be used in the
CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.

XX
SQ Sequence 2102 BP; 661 A; 419 C; 445 G; 577 T; 0 other;

Query Match 90.8%; Score 1356; DB 24; Length 2102;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
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Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
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Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
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Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
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Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
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Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
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Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
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Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
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Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

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Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
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Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
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Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
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Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
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Db   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||||||||||
Db   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
```

RESULT 6
AAN91043
ID AAN91043 standard; DNA; 2115 BP.
XX
AC AAN91043;
XX
DT 04-JUL-1990 (first entry)
XX
DE Decay accelerating factor (DAF) of clones lambda 33 and lambda 47.
XX
KW DAF; allograft rejection; affinity purification;
KW autoimmune disease; ds.
XX
OS Synthetic.
XX

| FH | Key | Location/Qualifiers |
|---|---|---|
| FT | CDS | 66..2015 |
| FT | | /*tag= a |
| FT | mat_peptide | 198..1208 |
| FT | | /*tag= b |
| FT | misc_signal | 1146 |
| FT | | /*tag= c |
| FT | | label= mRNA splice site. |

XX
PN WO8901041-A.
XX
PD 09-FEB-1989.
XX
PF 03-AUG-1988; 88WO-US02648.
XX
PR 06-AUG-1987; 87US-0083757.
XX
PA (GETH ) GENETECH INC.
XX
PI Caras I;
XX
DR WPI; 1989-061177/08.
DR P-PSDB; AAP94773.
XX
PT Fusion polypeptide for targeting protein to cell membrane -
PT comprisesphospholipid anchor domain with heterologous
PT polypeptide.
XX
PS Disclosure; ; 61pp; English.
XX
CC Recombinant DAF's are useful in treatment of inflamatory or cell lytic
CC autoimmune diseases and allograft rejection. Useful in diagnostic
CC compositions or in affinity purification.
XX
SQ Sequence 2115 BP; 682 A; 419 C; 446 G; 568 T; 0 other;

Query Match 90.8%; Score 1356; DB 10; Length 2115;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
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Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
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Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
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Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
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Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964
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Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

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Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

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Db   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
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Db   1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
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Db   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||||||||||
Db   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
```

RESULT 7
AAQ79863
ID  AAQ79863 standard; cDNA; 2115 BP.
XX
AC  AAQ79863;
XX
DT  23-JUL-1995  (first entry)
XX
DE  Decay accelerating factor cDNA.
XX
KW  Decay accelerating factor; DAF; mDAF; fusion protein; liposome;
KW  cell targeting; glycophosphatidylinositol; GPI; drug delivery; ds.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  CDS             66..1211
FT                  /*tag= a
FT  sig_peptide     66..167
FT                  /*tag= b
FT  mat_peptide     168..1208
FT                  /*tag= c
FT                  /product= mature mDAF protein
XX
PN  US5374548-A.
XX
PD  20-DEC-1994.
XX
PF  02-MAY-1986;  86US-0859107.
XX
PR  02-MAY-1986;  86US-0859107.
PR  06-AUG-1987;  87US-0083757.
PR  19-DEC-1991;  91US-0811048.
PR  12-FEB-1993;  93US-0017934.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Caras IW;
XX
DR  WPI; 1995-035649/05.
DR  P-PSDB; AAR66683.
XX
PT  Liposome(s) for targetting particular cells contg. fusion protein
PT  - of glyco:phosphatidyl:inositol anchor and heterologous
PT  targetting protein, e.g. for delivering toxins to infected or
PT  cancer cells.
XX
PS  Disclosure; Fig. 1a-1f; 36pp; English.
XX
CC  A probe (given in AAQ79865) based on the N-terminal sequence of human
CC  decay accelerating factor (DAF) was used to screen a HeLa cell
CC  lambda cDNA library.  Isolated clones encoding membrane-bound DAF
CC  (mDAF) were obtained, and the full sequence of mDAF cDNA was
CC  determined (AAQ79863).  The GPI signal domain of mDAF may be fused to
CC  a heterologous protein and targeted to cell membrane surfaces.
XX
SQ  Sequence 2115 BP; 675 A; 419 C; 446 G; 575 T; 0 other;

Query Match  90.8%;  Score 1356;  DB 16;  Length 2115;
Best Local Similarity  100.0%;  Pred. No. 0;
Matches 1356;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```
Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844
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Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||||||||||
Db   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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RESULT 8
AAH34999
ID AAH34999 standard; cDNA; 2302 BP.
XX
AC AAH34999;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2081.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 1; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG75594.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3567; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 2302 BP; 727 A; 486 C; 479 G; 609 T; 1 other;

Query Match 90.8%; Score 1356; DB 22; Length 2302;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 232

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 292

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 352

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 412

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    413 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 472

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    473 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 532

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    533 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 592

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    593 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 652

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    653 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 712

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    713 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 772

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    773 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 832

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    833 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 892

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    893 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 952

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    953 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 1012

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1013 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1072

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1073 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1132

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1133 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1192

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1193 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1252

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1253 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1312

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1313 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1372

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1373 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1432

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1433 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1492

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
          |||||||||||||||||||||||||||||||||||
Db   1493 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1528
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RESULT 9
AAH23076
ID  AAH23076 standard; DNA; 2263 BP.
XX
AC  AAH23076;
XX
DT  17-SEP-2001  (first entry)
XX
DE  Osteoarthritis tissue-derived nucleic acid sequence #6.
XX
KW  Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;
KW  wound healing; osteopathic; anti-arthritic, anti-inflammatory;
KW  vulnerary; antibacterial; antiallergic; ds.
XX
OS  Homo sapiens.
XX
PN  WO200153531-A2.
XX
PD  26-JUL-2001.
XX
PF  18-JAN-2001; 2001WO-US00016.
XX
PR  18-JAN-2000; 2000US-0176523.
XX
PA  (PHAA ) PHARMACIA CORP.
XX
PI  Phippard D,  Vasanthakamur G,  Dotson S,  Ma X;
XX
DR  WPI; 2001-451914/48.
XX
PT  Substantially purified protein, polypeptide or their fragments, used to
PT  identify a biologically active compound or composition and treat
PT  mammalian osteoarthritis  -
XX
PS  Claim 1; Page 93-95; 144pp; English.
XX
CC  Sequences AAH23071-23152 represent nucleic acid sequences derived from
CC  osteoarthritis tissues. The sequences are useful as probes and for the
CC  diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides
CC  and polypeptides of the invention are useful for generating diagnostic
CC  reagents, as targets for small molecule drug development, generation of
CC  therapeutics, and cloning genes. Specific antibodies are used to generate
CC  enzyme linked immunosorbent assays for detection of osteoarthritis. The
CC  invented molecules can be used to treat osteoarthritis or to analyse the
CC  disease-modifying activity of osteoarthritis drugs. Other disorders
CC  treatable using the nucleic acid sequences include atopic, inflammatory
CC  and infectious disorders e.g. Crohn's disease and sepsis, and wound
CC  healing.
XX
SQ  Sequence 2263 BP; 706 A; 475 C; 474 G; 607 T; 1 other;

  Query Match             82.1%;  Score 1226;  DB 22;  Length 2263;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy    148 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 207
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 220

Qy    208 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 267
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 280

Qy    268 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 327
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 340

Qy    328 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 387
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 400

Qy    388 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 447
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 460

Qy    448 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 507
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 520

Qy    508 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 567
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 580

Qy    568 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 627
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 640

Qy    628 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 687
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    641 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 700

Qy    688 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 747
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 760

Qy    748 GCAACCAT-CTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 806
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 GCAACCATGCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 820
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Qy     807 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 866
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     821 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 880

Qy     867 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 926
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     881 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 940

Qy     927 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 986
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     941 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 1000

Qy     987 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1046
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1001 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1060

Qy    1047 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1106
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1061 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1120

Qy    1107 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1121 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1180

Qy    1167 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1181 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1240

Qy    1227 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1241 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1300

Qy    1287 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1301 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1360

Qy    1347 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1361 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1420

Qy    1407 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1421 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1480

Qy    1467 CTTTAAGATGTGTTAGGAATGTCAACA 1493
           |||||||||||||||||||||||||||
Db    1481 CTTTAAGATGTGTTAGGAATGTCAACA 1507
```

```
RESULT 10
AAQ99105
ID   AAQ99105 standard; cDNA to mRNA; 2096 BP.
XX
AC   AAQ99105;
XX
DT   20-DEC-1995  (first entry)
XX
DE   Human DAF cDNA.
XX
KW   Chimeric complement inhibitor; C3 inhibitor; transplantation;
KW   transgenic animal; gene therapy; DAF; decay acceleration factor;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..1199
FT                   /*tag=  a
FT   sig_peptide     54..155
FT                   /*tag=  b
FT   mat_peptide     156..1196
FT                   /*tag=  c
XX
```

```
PN   WO9523856-A1.
XX
PD   08-SEP-1995.
XX
PF   01-MAR-1995;   95WO-US02945.
XX
PR   03-MAR-1994;   94US-0205508.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Fodor WL,  Rollins S,  Squinto SP;
XX
DR   WPI; 1995-320571/41.
XX
PT   Chimeric proteins having both C3 and C5b-9 complement inhibitory
PT   activity - useful for protecting non-human organs against complement
PT   attack, e.g. in transplantation
XX
PS   Disclosure; Page 45-47; 83pp; English.
XX
CC   Chimeric complement inhibitor proteins (CIPs) comprise: a functional
CC   domain (FD) having complement C3 inhibitory activity, e.g. human
CC   mature DAF (encoded by the sequence given in AAQ99105) or MCP
CC   (AAQ99106); and a FD having C5b-9 inhibitory activity, e.g. human
CC   mature CD59 (AAQ99104), non-human primate C5b-9 inhibitors (AAQ99107-11)
CC   or mature HVS-15 inhibitor (AAQ99112).  The CIPs allow safe,
CC   effective xerotransplantation of transgenic animal organs
CC   expressing such proteins into humans.
XX
SQ   Sequence 2096 BP; 671 A; 416 C; 439 G; 570 T; 0 other;
```

```
  Query Match             80.0%;  Score 1195;  DB 16;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy     206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy    1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy    1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
           ||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
```

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RESULT 11
AAT84471
ID   AAT84471 standard; cDNA to mRNA; 2096 BP.
XX
AC   AAT84471;
XX
DT   17-NOV-1997  (first entry)
XX
DE   Human DAF cDNA.
XX
KW   DAF; decay accelerating factor; human; C3 complement inhibitor;
KW   retrovirus; vector; gene therapy; stem cell; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..1199
FT                   /*tag=  a
FT   sig_peptide     54..155
FT                   /*tag=  b
FT   mat_peptide     156..1196
FT                   /*tag=  c
XX
PN   US5643770-A.
XX
PD   01-JUL-1997.
XX
PF   21-JUL-1994;   94US-0278630.
XX
PR   21-JUL-1994;   94US-0278630.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Mason JM,  Squinto SP;
XX
DR   WPI; 1997-350243/32.
DR   P-PSDB; AAW26317.
XX
PT   Retroviral vector particle expressing complement inhibitor activity
PT   - for transducing cells in body fluids containing complement
XX
PS   Disclosure; Column 41-46; 32pp; English.
XX
CC   This cDNA clone codes for human decay accelerating factor (DAF)
CC   (AAW26317), a protein that has C3 complement inhibitor activity.
CC   Claimed retroviral vector particles express a complement inhibitor
CC   such as DAF, and are thereby protected from inactivation upon
CC   exposure to body fluids containing complement. Also claimed are: (1)
CC   a producer cell producing the vector particle; and (2) a chimeric
CC   retroviral envelope protein (see also AAW26326) with at least part of
CC   the N-terminal receptor-binding domain removed and replaced by a
CC   protein domain having a complement inhibitor activity.  The vector
CC   is used in a claimed method for transducing cells in the presence of
CC   a body fluid containing complement, preferably ex vivo, especially
CC   for gene therapy, e.g. of hereditary or acquired blood disorders by
CC   transduction of haematopoietic stem cells.
XX
SQ   Sequence 2096 BP; 671 A; 416 C; 439 G; 570 T; 0 other;
```

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  Query Match             80.0%;  Score 1195;  DB 18;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy     206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420
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Qy     566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy    1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy    1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
           ||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
```

RESULT 12
AAV08935
ID  AAV08935 standard; cDNA to mRNA; 1146 BP.
XX
AC  AAV08935;
XX
DT  01-MAR-1999  (first entry)
XX
DE  DAF protein coding sequence.
XX
KW  DAF; decay accelerating factor; human; compliment protein; gene therapy;
KW  viral vector; ds.
XX
OS  Homo sapiens.
XX
PN  JP10313865-A.
XX
PD  02-DEC-1998.
XX
PF  15-MAY-1997;  97JP-0125965.
XX
PR  15-MAY-1997;  97JP-0125965.
XX
PA  (DINA-) DINABEKKU KENKYUSHO KK.
XX
DR  WPI; 1999-074147/07.
DR  P-PSDB; AAW73505.
XX
PT  Vector having complement controlling factor - useful for gene
PT  therapy
XX
PS  Example 3; Page 8-9; 15pp; Japanese.
XX
CC  This sequence encodes the human decay accelerating factor (DAF) protein.
CC  DAF can be used in the viral vector of the invention. The viral vector
CC  contains a factor controlling the function of a human complement protein,
CC  particularly a membrane combining type protein. The viral vector, which
CC  is stable in situ, is useful for gene therapy.
XX
SQ  Sequence 1146 BP; 325 A; 277 C; 260 G; 284 T; 0 other;

Query Match 76.8%; Score 1146; DB 20; Length 1146;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     199 ATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGG 258
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGG 60

Qy     259 CTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCA 318
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCA 120

Qy     319 GATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTA 378
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTA 180

Qy     379 ATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATC 438
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATC 240

Qy     439 TGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTG 498
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTG 300

Qy     499 CCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCA 558
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCA 360

Qy     559 GTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCA 618
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCA 420

Qy     619 CCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAG 678
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAG 480

Qy     679 AAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATA 738
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATA 540
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Qy     739 TTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACT 798
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACT 600

Qy     799 TCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGC 858
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGC 660

Qy     859 AGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGT 918
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGT 720

Qy     919 GACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATT 978
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATT 780

Qy     979 GGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCA 1038
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCA 840

Qy    1039 CCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACC 1098
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACC 900

Qy    1099 ACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACC 1158
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACC 960

Qy    1159 ACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTT 1218
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTT 1020

Qy    1219 CATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCT 1278
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCT 1080

Qy    1279 GGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTG 1338
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTG 1140

Qy    1339 ACTTAG 1344
           ||||||
Db    1141 ACTTAG 1146
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RESULT 13
AAN70048
ID   AAN70048 standard; DNA; 2233 BP.
XX
AC   AAN70048;
XX
DT   03-OCT-2002  (updated)
DT   03-FEB-1991  (first entry)
XX
DE   Encodes human decay acceleration factor variant #2.
XX
KW   Decay acceleration factor; sDAF; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     66..1388
FT                   /*tag=  a
FT                   /product=sDAF
XX
PN   EP244267-A.
XX
PD   04-NOV-1987.
XX
PF   01-MAY-1987;   87EP-0303944.
XX
PR   02-MAY-1986;   86US-0859107.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1987-308481/44.
DR   P-PSDB; AAP70049.
XX
PT   New decay accelerating factor variants - obtained with the factor by
PT   using recombinant DNA procedures.
XX
PS   Disclosure; Page 18-20; 20pp; English.
XX
CC   The cDNA sequence is that of clones phage lambda 33 (to the
CC   HindIII site at residue 1) and phage lambda 41 (HindIII to
CC   the 3' end) encoding a variant of DAF (sDAF).  DAF and
CC   variants are useful for treating paraoxysmal nocturnal
CC   haemoglobinuria, or inflammatory or cell lytic autoimmune
CC   diseases.  They may be used to ameliorate allograft
CC   rejection or autoimmune diseases.  See also AAN70046, AAN70047.
CC   (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ   Sequence 2233 BP; 695 A; 455 C; 475 G; 608 T; 0 other;
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  Query Match             76.6%;  Score 1143;  DB 8;  Length 2233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGG 1280
          |||
Db   1145 TGG 1147
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RESULT 14
AAN91044
ID   AAN91044 standard; DNA; 2233 BP.
XX
AC   AAN91044;
XX
DT   04-JUL-1990  (first entry)
XX
DE   Membrane bound decay accelerating factor (sDAF).
XX
KW   DAF; allograft rejection; affinity purification;
KW   autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1385
FT                   /*tag=  a
FT   mat_peptide     168..1385
FT                   /*tag=  b
XX
PN   WO8901041-A.
XX
PD   09-FEB-1989.
XX
PF   03-AUG-1988;   88WO-US02648.
XX
PR   06-AUG-1987;   87US-0083757.
XX
PA   (GETH ) GENETECH INC.
XX
PI   Caras I;
XX
DR   WPI; 1989-061177/08.
DR   P-PSDB; AAP94774.
XX
PT   Fusion polypeptide for targeting protein to cell membrane -
PT   comprisesphospholipid anchor domain with heterologous
PT   polypeptide.
XX
PS   Disclosure; ; 61pp; English.
XX
CC   Recombinant DAF's are useful in treatment of inflamatory or cell lytic
CC   autoimmune diseases and allograft rejection. Useful in diagnostic
CC   compositions or in affinity purification.
CC   CDS differs from the mature peptide by sequence encoding the secretory
CC   leader.
XX
SQ   Sequence 2233 BP; 695 A; 455 C; 476 G; 607 T; 0 other;

  Query Match             76.6%;  Score 1143;  DB 10;  Length 2233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
```

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGG 1280
          |||
Db   1145 TGG 1147
```

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RESULT 15
AAQ79864
ID   AAQ79864 standard; cDNA; 2233 BP.
XX
AC   AAQ79864;
XX
DT   23-JUL-1995  (first entry)
XX
DE   Decay accelerating factor cDNA.
XX
KW   Decay accelerating factor; DAF; sDAF; fusion protein; liposome;
KW   cell targeting; glycophosphatidylinositol; GPI; drug delivery; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1388
FT                   /*tag=  a
FT   sig_peptide     66..167
FT                   /*tag=  b
FT   mat_peptide     168..1385
FT                   /*tag=  c
FT                   /product= mature sDAF protein
XX
PN   US5374548-A.
XX
PD   20-DEC-1994.
XX
PF   02-MAY-1986;   86US-0859107.
XX
PR   02-MAY-1986;   86US-0859107.
PR   06-AUG-1987;   87US-0083757.
PR   19-DEC-1991;   91US-0811048.
PR   12-FEB-1993;   93US-0017934.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1995-035649/05.
DR   P-PSDB; AAR66684.
XX
PT   Liposome(s) for targetting particular cells contg. fusion protein
PT    - of glyco:phosphatidyl:inositol anchor and heterologous
PT   targetting protein, e.g. for delivering toxins to infected or
PT   cancer cells.
XX
PS   Disclosure; Fig. 2a-2g; 36pp; English.
XX
CC   A probe (given in AAQ79865) based on the N-terminal sequence of human
CC   decay accelerating factor (DAF) was used to screen a HeLa cell
CC   lambda cDNA library.  Isolated clones encoding soluble DAF
CC   (sDAF) were obtained; the full sequence of sDAF cDNA is given in
CC   AAQ79864 and the deduced protein sequence in AAR66684.
XX
SQ   Sequence 2233 BP; 695 A; 456 C; 474 G; 608 T; 0 other;
```

```
  Query Match             76.6%;  Score 1143;  DB 16;  Length 2233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
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Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
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Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
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Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
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Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
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Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
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Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
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Qy   1278 TGG 1280
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Db   1145 TGG 1147
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Search completed: February 24, 2003, 02:48:57
Job time : 338.627 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 01:55:27 ; Search time 3863.53 Seconds
(without alignments)
11246.328 Million cell updates/sec

Title: US-09-623-035-5
Perfect score: 1493
Sequence: 1 tttaaacgggccctctagac.....atgtgttaggaatgtcaaca 1493

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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31: em_htg_inv:*
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36: em_htg_mam:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
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| | 1 | 1493 | 100.0 | 1493 | 6 | AX018850 | AX018850 Sequence |
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| | 3 | 1356 | 90.8 | 2102 | 6 | AX333057 | AX333057 Sequence |
| | 4 | 1356 | 90.8 | 2102 | 9 | HUMDAFB | M31516 Human decay |
| | 5 | 1356 | 90.8 | 2115 | 6 | I05091 | I05091 Sequence 2 |
| | 6 | 1356 | 90.8 | 2115 | 6 | I09215 | I09215 Sequence 1 |
| | 7 | 1310 | 87.7 | 1357 | 9 | BC001288 | BC001288 Homo sapi |
| | 8 | 1226 | 82.1 | 2263 | 6 | AX202076 | AX202076 Sequence |
| | 9 | 1195 | 80.0 | 2096 | 6 | I41330 | I41330 Sequence 1 |
| | 10 | 1195 | 80.0 | 2096 | 6 | I49078 | I49078 Sequence 1 |
| | 11 | 1195 | 80.0 | 2096 | 6 | I50941 | I50941 Sequence 10 |
| | 12 | 1143 | 76.6 | 2220 | 9 | HUMDAFA | M30142 Human decay |
| | 13 | 1143 | 76.6 | 2233 | 6 | I09216 | I09216 Sequence 3 |
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| | 15 | 1097 | 73.5 | 2237 | 6 | A65264 | A65264 Sequence 1 |
| | 16 | 1092 | 73.1 | 2233 | 6 | I05094 | I05094 Sequence 5 |
| | 17 | 1040 | 69.7 | 1313 | 9 | HSU88576 | U88576 Human decay |
| | 18 | 1023 | 68.5 | 1735 | 9 | AF052110 | AF052110 Homo sapi |
| | 19 | 970 | 65.0 | 1848 | 6 | AX134168 | AX134168 Sequence |
| | 20 | 970 | 65.0 | 1878 | 6 | AR031710 | AR031710 Sequence |
| | 21 | 816 | 54.7 | 969 | 6 | AR066586 | AR066586 Sequence |
| | 22 | 816 | 54.7 | 969 | 6 | I70309 | I70309 Sequence 12 |
| | 23 | 707 | 47.4 | 860 | 6 | AR066589 | AR066589 Sequence |
| | 24 | 707 | 47.4 | 860 | 6 | I70312 | I70312 Sequence 19 |
| | 25 | 677 | 45.3 | 925 | 9 | AY055759 | AY055759 Homo sapi |
| | 26 | 668 | 44.7 | 1266 | 9 | AF149760 | AF149760 Pan trogl |
| | 27 | 594 | 39.8 | 1515 | 9 | AY055760 | AY055760 Homo sapi |
| | 28 | 594 | 39.8 | 2162 | 9 | AY055758 | AY055758 Homo sapi |
| | 29 | 520 | 34.8 | 559 | 6 | AX018849 | AX018849 Sequence |
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| | 31 | 434 | 29.1 | 1140 | 9 | AF149761 | AF149761 Pan trogl |
| | 32 | 393 | 26.3 | 586 | 6 | AX018848 | AX018848 Sequence |
| | 33 | 354 | 23.7 | 1864 | 9 | AY055757 | AY055757 Homo sapi |
| c | 34 | 279 | 18.7 | 586 | 6 | AX335240 | AX335240 Sequence |
| | 35 | 238 | 15.9 | 1245 | 9 | S67775 | S67775 decay-accel |
| c | 36 | 221 | 14.8 | 224 | 6 | AX341675 | AX341675 Sequence |
| | 37 | 215 | 14.4 | 1077 | 6 | AX014893 | AX014893 Sequence |
| | 38 | 215 | 14.4 | 141124 | 9 | AL391597 | AL391597 Human DNA |
| | 39 | 215 | 14.4 | 142672 | 2 | AL355527 | AL355527 Homo sapi |
| | 40 | 215 | 14.4 | 167359 | 2 | AC031978 | AC031978 Homo sapi |
| | 41 | 192 | 12.9 | 130935 | 9 | AL596218 | AL596218 Human DNA |
| | 42 | 192 | 12.9 | 150933 | 2 | AC010829 | AC010829 Homo sapi |
| c | 43 | 186 | 12.5 | 375 | 11 | G28412 | G28412 human STS S |
| | 44 | 165 | 11.1 | 2003 | 9 | HUMDAFC1 | M64356 Human decay |
| | 45 | 149 | 10.0 | 400 | 11 | G11240 | G11240 human STS S |
| | 46 | 115 | 7.7 | 747 | 6 | AR016516 | AR016516 Sequence |
| | 47 | 115 | 7.7 | 747 | 6 | AR096899 | AR096899 Sequence |
| | 48 | 114 | 7.6 | 134 | 6 | AR016512 | AR016512 Sequence |
| c | 49 | 114 | 7.6 | 134 | 6 | AR016513 | AR016513 Sequence |
| | 50 | 114 | 7.6 | 134 | 6 | AR096895 | AR096895 Sequence |
| c | 51 | 114 | 7.6 | 134 | 6 | AR096896 | AR096896 Sequence |
| | 52 | 114 | 7.6 | 300 | 6 | AR016514 | AR016514 Sequence |
| | 53 | 114 | 7.6 | 300 | 6 | AR096897 | AR096897 Sequence |
| | 54 | 114 | 7.6 | 314 | 6 | I64711 | I64711 Sequence 1 |
| | 55 | 114 | 7.6 | 314 | 6 | I64712 | I64712 Sequence 3 |
| | 56 | 114 | 7.6 | 314 | 6 | I64713 | I64713 Sequence 4 |
| | 57 | 114 | 7.6 | 786 | 6 | AR016518 | AR016518 Sequence |
| | 58 | 114 | 7.6 | 786 | 6 | AR096901 | AR096901 Sequence |
| | 59 | 109 | 7.3 | 674 | 9 | AB003312 | AB003312 Homo sapi |
| | 60 | 109 | 7.3 | 674 | 9 | AB003313 | AB003313 Pan trogl |
| | 61 | 109 | 7.3 | 674 | 9 | AB003314 | AB003314 Pongo pyg |
| | 62 | 107 | 7.2 | 989 | 6 | I64714 | I64714 Sequence 5 |
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| | 65 | 84 | 5.6 | 662 | 9 | AB003317 | AB003317 Hylobates |

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| | 66 | 76 | 5.1 | 1250 | 9 | AF149762 AF149762 Papio ham |
| | 67 | 76 | 5.1 | 1250 | 9 | AF149763 AF149763 Macaca mu |
| | 68 | 68 | 4.6 | 1034 | 9 | AF149766 AF149766 Erythroce |
| | 69 | 68 | 4.6 | 1055 | 9 | AF149765 AF149765 Erythroce |
| | 70 | 68 | 4.6 | 1250 | 9 | AF149764 AF149764 Erythroce |
| | 71 | 68 | 4.6 | 1250 | 9 | AF149767 AF149767 Erythroce |
| | 72 | 64 | 4.3 | 883 | 9 | S51407 S51407 decay accel |
| | 73 | 46 | 3.1 | 848 | 9 | AB003318 AB003318 Ateles ge |
| c | 74 | 44 | 2.9 | 44 | 6 | I41346 I41346 Sequence 17 |
| c | 75 | 44 | 2.9 | 44 | 6 | I49094 I49094 Sequence 17 |
| | 76 | 43 | 2.9 | 761 | 9 | AB003315 AB003315 Macaca fu |
| c | 77 | 40 | 2.7 | 479 | 6 | AX261635 AX261635 Sequence |
| | 78 | 39 | 2.6 | 39 | 6 | I41345 I41345 Sequence 16 |
| | 79 | 39 | 2.6 | 39 | 6 | I49093 I49093 Sequence 16 |
| | 80 | 34 | 2.3 | 35 | 6 | AX134149 AX134149 Sequence |
| c | 81 | 34 | 2.3 | 1241 | 6 | AX460911 AX460911 Sequence |
| c | 82 | 34 | 2.3 | 1566 | 6 | AX455878 AX455878 Sequence |
| c | 83 | 34 | 2.3 | 4291 | 12 | AF302189 AF302189 Synthetic |
| c | 84 | 33 | 2.2 | 1266 | 6 | AX455875 AX455875 Sequence |
| c | 85 | 33 | 2.2 | 1329 | 6 | AX455876 AX455876 Sequence |
| c | 86 | 33 | 2.2 | 1395 | 6 | AX455877 AX455877 Sequence |
| c | 87 | 33 | 2.2 | 1542 | 6 | AX455874 AX455874 Sequence |
| c | 88 | 33 | 2.2 | 5771 | 12 | AF060226 AF060226 Eukaryoti |
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| c | 90 | 33 | 2.2 | 6567 | 6 | AX128350 AX128350 Sequence |
| c | 91 | 33 | 2.2 | 6623 | 6 | AX128345 AX128345 Sequence |
| c | 92 | 33 | 2.2 | 6625 | 12 | AF191496 AF191496 Cloning v |
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| c | 94 | 33 | 2.2 | 6649 | 6 | AX180726 AX180726 Sequence |
| c | 95 | 33 | 2.2 | 6695 | 6 | AX128347 AX128347 Sequence |
| c | 96 | 33 | 2.2 | 6695 | 6 | AX128353 AX128353 Sequence |
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| c | 99 | 33 | 2.2 | 6818 | 6 | AX128346 AX128346 Sequence |
| c | 100 | 33 | 2.2 | 6828 | 6 | AX128340 AX128340 Sequence |
| c | 101 | 33 | 2.2 | 6833 | 6 | AX128349 AX128349 Sequence |
| c | 102 | 33 | 2.2 | 6900 | 6 | AX128341 AX128341 Sequence |
| c | 103 | 33 | 2.2 | 6956 | 6 | AX128348 AX128348 Sequence |
| c | 104 | 33 | 2.2 | 7038 | 6 | AX128342 AX128342 Sequence |
| | 105 | 33 | 2.2 | 7475 | 6 | AX001323 AX001323 Sequence |
| | 106 | 33 | 2.2 | 7475 | 6 | E36259 E36259 Human semap |
| | 107 | 33 | 2.2 | 8192 | 6 | AX001324 AX001324 Sequence |
| | 108 | 33 | 2.2 | 8192 | 6 | E36260 E36260 Human semap |
| c | 109 | 32 | 2.1 | 72 | 6 | AX381646 AX381646 Sequence |
| c | 110 | 32 | 2.1 | 127 | 6 | BD000578 BD000578 DNA const |
| c | 111 | 32 | 2.1 | 396 | 6 | AX093183 AX093183 Sequence |
| | 112 | 32 | 2.1 | 420 | 6 | AR166291 AR166291 Sequence |
| | 113 | 32 | 2.1 | 438 | 6 | AX156356 AX156356 Sequence |
| c | 114 | 32 | 2.1 | 482 | 6 | AX321950 AX321950 Sequence |
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| | 116 | 32 | 2.1 | 707 | 6 | AX093377 AX093377 Sequence |
| | 117 | 32 | 2.1 | 746 | 9 | AB003319 AB003319 Cebus ape |
| c | 118 | 32 | 2.1 | 998 | 6 | AX381968 AX381968 Sequence |
| c | 119 | 32 | 2.1 | 1247 | 6 | AX455873 AX455873 Sequence |
| | 120 | 32 | 2.1 | 1438 | 4 | AF228060 AF228060 Sus scrof |
| | 121 | 32 | 2.1 | 1546 | 4 | AF228059 AF228059 Sus scrof |
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| | 123 | 32 | 2.1 | 1637 | 6 | AX014811 AX014811 Sequence |
| | 124 | 32 | 2.1 | 1954 | 4 | AF228061 AF228061 Sus scrof |
| c | 125 | 32 | 2.1 | 2001 | 6 | AX058020 AX058020 Sequence |
| c | 126 | 32 | 2.1 | 2004 | 6 | AX150386 AX150386 Sequence |
| c | 127 | 32 | 2.1 | 2004 | 6 | AX191639 AX191639 Sequence |
| c | 128 | 32 | 2.1 | 2010 | 6 | AX058018 AX058018 Sequence |
| c | 129 | 32 | 2.1 | 2055 | 6 | AX191654 AX191654 Sequence |
| c | 130 | 32 | 2.1 | 2247 | 6 | AX150388 AX150388 Sequence |
| c | 131 | 32 | 2.1 | 2247 | 6 | AX191641 AX191641 Sequence |
| | 132 | 32 | 2.1 | 3373 | 6 | AX455691 AX455691 Sequence |
| c | 133 | 32 | 2.1 | 4488 | 6 | AX191651 AX191651 Sequence |
| c | 134 | 32 | 2.1 | 5082 | 6 | A91754 A91754 Sequence 10 |
| c | 135 | 32 | 2.1 | 5432 | 6 | AX026821 AX026821 Sequence |
| c | 136 | 32 | 2.1 | 5650 | 6 | AX226281 AX226281 Sequence |
| c | 137 | 32 | 2.1 | 5731 | 6 | AX202478 AX202478 Sequence |
| c | 138 | 32 | 2.1 | 5953 | 6 | AX191649 AX191649 Sequence |
| c | 139 | 32 | 2.1 | 6082 | 6 | AX141045 AX141045 Sequence |
| c | 140 | 32 | 2.1 | 6082 | 6 | AX200905 AX200905 Sequence |
| c | 141 | 32 | 2.1 | 6082 | 6 | AX267561 AX267561 Sequence |
| c | 142 | 32 | 2.1 | 6253 | 6 | AR031374 AR031374 Sequence |
| c | 143 | 32 | 2.1 | 6439 | 6 | AX347593 AX347593 Sequence |
| c | 144 | 32 | 2.1 | 6452 | 6 | AX347592 AX347592 Sequence |
| c | 145 | 32 | 2.1 | 6801 | 6 | AX128352 AX128352 Sequence |
| c | 146 | 32 | 2.1 | 6801 | 6 | AX128355 AX128355 Sequence |
| c | 147 | 32 | 2.1 | 6980 | 6 | AX209897 AX209897 Sequence |
| c | 148 | 32 | 2.1 | 7076 | 6 | AX347587 AX347587 Sequence |
| c | 149 | 32 | 2.1 | 7076 | 6 | AX347588 AX347588 Sequence |
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| c | 151 | 32 | 2.1 | 7092 | 6 | AX347589 AX347589 Sequence |
| c | 152 | 32 | 2.1 | 7108 | 6 | AX001326 AX001326 Sequence |
| c | 153 | 32 | 2.1 | 7108 | 6 | E36262 E36262 Human semap |
| c | 154 | 32 | 2.1 | 7469 | 6 | AX209896 AX209896 Sequence |
| c | 155 | 32 | 2.1 | 7563 | 6 | AX209895 AX209895 Sequence |
| c | 156 | 32 | 2.1 | 7573 | 6 | AX347594 AX347594 Sequence |
| c | 157 | 32 | 2.1 | 8331 | 6 | AX026824 AX026824 Sequence |
| | 158 | 31 | 2.1 | 40 | 6 | I41347 I41347 Sequence 18 |
| | 159 | 31 | 2.1 | 40 | 6 | I49095 I49095 Sequence 18 |
| | 160 | 31 | 2.1 | 64 | 9 | S72858 S72858 DAF (Dr(a-) |
| c | 161 | 31 | 2.1 | 1210 | 6 | AX455461 AX455461 Sequence |
| | 162 | 31 | 2.1 | 1584 | 6 | AX050266 AX050266 Sequence |
| c | 163 | 30 | 2.0 | 33 | 6 | AX134148 AX134148 Sequence |
| | 164 | 30 | 2.0 | 40 | 9 | S70688 S70688 decay-accel |
| c | 165 | 30 | 2.0 | 686 | 6 | AX321981 AX321981 Sequence |
| c | 166 | 29 | 1.9 | 34 | 6 | I41348 I41348 Sequence 19 |
| c | 167 | 29 | 1.9 | 34 | 6 | I49096 I49096 Sequence 19 |
| c | 168 | 29 | 1.9 | 6253 | 6 | BD009742 BD009742 Compositi |
| | 169 | 27 | 1.8 | 150381 | 8 | AP003794 AP003794 Oryza sat |
| | 170 | 27 | 1.8 | 153666 | 8 | AP003287 AP003287 Oryza sat |
| | 171 | 26 | 1.7 | 33 | 6 | AR066582 AR066582 Sequence |
| | 172 | 26 | 1.7 | 33 | 6 | AR134338 AR134338 Sequence |
| | 173 | 26 | 1.7 | 33 | 6 | I70305 I70305 Sequence 8 |
| | 174 | 26 | 1.7 | 57 | 6 | AX360663 AX360663 Sequence |
| c | 175 | 26 | 1.7 | 1467 | 6 | AX249819 AX249819 Sequence |
| c | 176 | 26 | 1.7 | 168158 | 2 | AC125325 AC125325 Mus muscu |
| c | 177 | 26 | 1.7 | 237678 | 10 | AC055818 AC055818 Mus muscu |
| | 178 | 25 | 1.7 | 39 | 6 | AR066577 AR066577 Sequence |
| | 179 | 25 | 1.7 | 39 | 6 | I70300 I70300 Sequence 3 |
| | 180 | 25 | 1.7 | 56 | 6 | I82394 I82394 Sequence 30 |
| | 181 | 25 | 1.7 | 57 | 6 | AR098411 AR098411 Sequence |
| c | 182 | 25 | 1.7 | 57 | 6 | BD012891 BD012891 Nucleus l |
| c | 183 | 25 | 1.7 | 57 | 23 | BD008326 Bd008326 Nucleus l |
| | 184 | 25 | 1.7 | 59 | 6 | AX278155 AX278155 Sequence |
| c | 185 | 25 | 1.7 | 64 | 6 | AX381743 AX381743 Sequence |
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| c | 187 | 25 | 1.7 | 83 | 6 | AX146299 AX146299 Sequence |
| c | 188 | 25 | 1.7 | 446 | 6 | AX255952 AX255952 Sequence |
| c | 189 | 25 | 1.7 | 1369 | 6 | A89692 A89692 Sequence 5 |
| c | 190 | 25 | 1.7 | 1408 | 6 | AX461605 AX461605 Sequence |
| | 191 | 25 | 1.7 | 1466 | 8 | AY084934 AY084934 Arabidops |
| c | 192 | 25 | 1.7 | 6896 | 6 | AR031375 AR031375 Sequence |
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| | 199 | 25 | 1.7 | 187601 | 8 | OSJN00079 AL606645 Oryza sat |
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| | 207 | 24 | 1.6 | 58 | 6 | AR122569 AR122569 Sequence |
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| | 209 | 24 | 1.6 | 66 | 6 | AX448935 AX448935 Sequence |
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| | 219 | 24 | 1.6 | 375 | 8 | AF231782 AF231782 Pinus tae |
| | 220 | 24 | 1.6 | 587 | 8 | AF231772 AF231772 Pinus tae |
| | 221 | 24 | 1.6 | 587 | 8 | AF440260 AF440260 Pinus tae |
| c | 222 | 24 | 1.6 | 629 | 5 | GGU40041 U40041 Gallus gall |
| | 223 | 24 | 1.6 | 978 | 6 | AX014812 AX014812 Sequence |
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| | 225 | 24 | 1.6 | 227968 | 10 | AC098723 AC098723 Mus muscu |
| | 226 | 24 | 1.6 | 256345 | 2 | AC120552 AC120552 Mus muscu |
| c | 227 | 24 | 1.6 | 321914 | 2 | AC126554 AC126554 Mus muscu |
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| | 229 | 23 | 1.5 | 68 | 6 | AX458274 AX458274 Sequence |
| c | 230 | 23 | 1.5 | 288 | 11 | AU049384 AU049384 Rattus no |
| | 231 | 23 | 1.5 | 317 | 8 | AF231778 AF231778 Pinus tae |
| | 232 | 23 | 1.5 | 317 | 11 | AU026201 AU026201 Rattus no |
| | 233 | 23 | 1.5 | 359 | 8 | AF231781 AF231781 Pinus tae |
| | 234 | 23 | 1.5 | 387 | 8 | AF441510 AF441510 Pinus tae |
| c | 235 | 23 | 1.5 | 1590 | 6 | AX350853 AX350853 Sequence |
| c | 236 | 23 | 1.5 | 4944 | 6 | AX489272 AX489272 Sequence |
| c | 237 | 23 | 1.5 | 10172 | 6 | AX275027 AX275027 Sequence |
| c | 238 | 23 | 1.5 | 13104 | 6 | AR151479 AR151479 Sequence |
| | 239 | 23 | 1.5 | 34948 | 3 | CBRG33E23 AC084551 Caenorhab |
| | 240 | 23 | 1.5 | 46943 | 9 | AF165141 AF165141 Homo sapi |
| c | 241 | 23 | 1.5 | 61969 | 2 | AC014103 AC014103 Drosophil |
| | 242 | 23 | 1.5 | 66822 | 9 | AL606529 AL606529 Human DNA |
| c | 243 | 23 | 1.5 | 84606 | 2 | AC097978 AC097978 Rattus no |
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| | 245 | 23 | 1.5 | 101623 | 9 | AL450389 AL450389 Human DNA |
| | 246 | 23 | 1.5 | 107600 | 9 | AC084697 AC084697 Homo sapi |
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| | 248 | 23 | 1.5 | 123412 | 2 | AC121352 AC121352 Rattus no |
| | 249 | 23 | 1.5 | 126829 | 8 | OSJN00032 AL606619 Oryza sat |
| | 250 | 23 | 1.5 | 133461 | 2 | AC025968 AC025968 Homo sapi |
| c | 251 | 23 | 1.5 | 140026 | 2 | AP005324 AP005324 Oryza sat |
| | 252 | 23 | 1.5 | 145588 | 9 | AC010000 AC010000 Homo sapi |
| | 253 | 23 | 1.5 | 145819 | 2 | AC090255 AC090255 Homo sapi |
| | 254 | 23 | 1.5 | 148591 | 2 | AC097032 AC097032 Rattus no |
| c | 255 | 23 | 1.5 | 148724 | 2 | AC128927 AC128927 Rattus no |
| | 256 | 23 | 1.5 | 156232 | 2 | AC096392 AC096392 Rattus no |
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| | 258 | 23 | 1.5 | 164655 | 9 | AL449264 AL449264 Human DNA |
| | 259 | 23 | 1.5 | 168293 | 2 | AC027174 AC027174 Homo sapi |
| | 260 | 23 | 1.5 | 169271 | 3 | AC009916 AC009916 Drosophil |
| | 261 | 23 | 1.5 | 170394 | 2 | AC024371 AC024371 Homo sapi |
| c | 262 | 23 | 1.5 | 170429 | 2 | AC115735 AC115735 Mus muscu |
| | 263 | 23 | 1.5 | 177108 | 2 | AC110561 AC110561 Mus muscu |
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| | 270 | 23 | 1.5 | 187097 | 2 | AC113727 AC113727 Rattus no |
| c | 271 | 23 | 1.5 | 196926 | 2 | AL596125 AL596125 Mus muscu |
| c | 272 | 23 | 1.5 | 197171 | 2 | AC095245 AC095245 Rattus no |
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| | 274 | 23 | 1.5 | 198693 | 10 | AL672190 AL672190 Mouse DNA |
| c | 275 | 23 | 1.5 | 204127 | 2 | AC127153 AC127153 Rattus no |
| c | 276 | 23 | 1.5 | 215711 | 3 | AC008205 AC008205 Drosophil |
| c | 277 | 23 | 1.5 | 228479 | 3 | AE003749 AE003749 Drosophil |
| | 278 | 23 | 1.5 | 241429 | 2 | AL591854 AL591854 Mus muscu |
| | 279 | 23 | 1.5 | 242991 | 2 | AC107250 AC107250 Rattus no |
| | 280 | 23 | 1.5 | 243179 | 2 | AC123863 AC123863 Mus muscu |
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| c | 284 | 22 | 1.5 | 47 | 6 | I41342 I41342 Sequence 13 |
| c | 285 | 22 | 1.5 | 47 | 6 | I49090 I49090 Sequence 13 |
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| | 287 | 22 | 1.5 | 65 | 6 | AX483999 AX483999 Sequence |
| c | 288 | 22 | 1.5 | 158 | 6 | A06392 A06392 Synthetic n |
| c | 289 | 22 | 1.5 | 209 | 11 | G22350 G22350 human STS W |
| c | 290 | 22 | 1.5 | 217 | 5 | AF055429 AF055429 Oncorhync |
| | 291 | 22 | 1.5 | 243 | 11 | AF253636 AF253636 Sus scrof |
| c | 292 | 22 | 1.5 | 298 | 11 | HUMUT1047 L17755 Human STS U |
| c | 293 | 22 | 1.5 | 424 | 6 | AX255972 AX255972 Sequence |
| | 294 | 22 | 1.5 | 483 | 8 | AF169205 AF169205 Glycine m |
| c | 295 | 22 | 1.5 | 507 | 3 | AF461314 AF461314 Drosophil |
| | 296 | 22 | 1.5 | 544 | 9 | HSHZREP11 X59826 Human chrom |
| c | 297 | 22 | 1.5 | 688 | 6 | A86256 A86256 Sequence 91 |
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| c | 300 | 22 | 1.5 | 807 | 6 | AX381963 AX381963 Sequence |
| c | 301 | 22 | 1.5 | 1054 | 14 | SIAF003047 AF003047 Simian im |
| | 302 | 22 | 1.5 | 1164 | 10 | CG12BS X79297 C.griseus r |
| c | 303 | 22 | 1.5 | 1226 | 5 | CCU64803 U64803 Coturnix co |
| c | 304 | 22 | 1.5 | 1308 | 8 | OSMYB1308 Y11352 O.sativa mR |
| c | 305 | 22 | 1.5 | 1497 | 3 | DME011672 AJ011672 Drosophil |
| | 306 | 22 | 1.5 | 1624 | 9 | HUMRSDNFA M29891 Human small |
| c | 307 | 22 | 1.5 | 1951 | 3 | AY070499 AY070499 Drosophil |
| c | 308 | 22 | 1.5 | 1968 | 10 | MMU46463 U46463 Mus musculu |
| | 309 | 22 | 1.5 | 2067 | 9 | AK098087 AK098087 Homo sapi |
| c | 310 | 22 | 1.5 | 2190 | 6 | AR174768 AR174768 Sequence |
| c | 311 | 22 | 1.5 | 3276 | 3 | AF465312 AF465312 Dictyoste |
| | 312 | 22 | 1.5 | 4093 | 10 | RATRHL1 K02817 Rat asialog |
| c | 313 | 22 | 1.5 | 4887 | 3 | AB010299 AB010299 Drosophil |
| c | 314 | 22 | 1.5 | 6140 | 6 | AX141046 AX141046 Sequence |
| c | 315 | 22 | 1.5 | 6140 | 6 | AX200906 AX200906 Sequence |
| c | 316 | 22 | 1.5 | 6140 | 6 | AX267562 AX267562 Sequence |
| c | 317 | 22 | 1.5 | 6147 | 6 | AX403980 AX403980 Sequence |
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| | 319 | 22 | 1.5 | 8331 | 9 | HSU28054 U28054 Homo sapien |
| c | 320 | 22 | 1.5 | 8659 | 2 | AC117270 AC117270 Dictyoste |
| c | 321 | 22 | 1.5 | 8750 | 6 | AX209898 AX209898 Sequence |
| | 322 | 22 | 1.5 | 8934 | 10 | MUSBB2R L27595 Mus muscari |
| c | 323 | 22 | 1.5 | 11940 | 2 | AC022158 AC022158 Homo sapi |
| c | 324 | 22 | 1.5 | 13987 | 10 | AB015749 AB015749 Rattus no |
| c | 325 | 22 | 1.5 | 17799 | 2 | AC017128 AC017128 Drosophil |
| c | 326 | 22 | 1.5 | 20163 | 2 | AC017907 AC017907 Drosophil |
| c | 327 | 22 | 1.5 | 24232 | 3 | CEC03E10 Z81458 Caenorhabdi |
| | 328 | 22 | 1.5 | 24833 | 9 | AP001973 AP001973 Homo sapi |
| c | 329 | 22 | 1.5 | 27302 | 2 | AC020017 AC020017 Drosophil |
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| c | 331 | 22 | 1.5 | 40557 | 2 | AC130959 AC130959 Rattus no |
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| | 333 | 22 | 1.5 | 53000 | 9 | AP002990 AP002990 Homo sapi |
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| | 346 | 22 | 1.5 | 68720 | 2 | AC120411 AC120411 Mus muscu |
| c | 347 | 22 | 1.5 | 69024 | 2 | AC111384 AC111384 Rattus no |
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| | 351 | 22 | 1.5 | 76607 | 2 | AC124647 AC124647 Mus muscu |
| c | 352 | 22 | 1.5 | 80692 | 2 | AC100569 AC100569 Mus muscu |
| c | 353 | 22 | 1.5 | 81962 | 2 | AC128396 AC128396 Rattus no |
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| | 355 | 22 | 1.5 | 88003 | 2 | AC111470 AC111470 Rattus no |
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| | 357 | 22 | 1.5 | 94096 | 2 | AP004081 AP004081 Oryza sat |

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| c | 358 | 22 | 1.5 | 94206 | 2 | AC129755 |
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| c | 362 | 22 | 1.5 | 100141 | 2 | AC091426 |
| | 363 | 22 | 1.5 | 100181 | 2 | AC097039 |
| | 364 | 22 | 1.5 | 100450 | 2 | AC094545 |
| c | 365 | 22 | 1.5 | 101333 | 2 | AC112437 |
| | 366 | 22 | 1.5 | 102926 | 9 | AC004230 |
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| | 370 | 22 | 1.5 | 106441 | 9 | HSJ803J11 |
| | 371 | 22 | 1.5 | 110000 | 2 | AC099209_0 |
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| | 374 | 22 | 1.5 | 110000 | 2 | LMFLCHR32_08 |
| c | 375 | 22 | 1.5 | 110000 | 2 | LMFLCHR36_11 |
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| | 381 | 22 | 1.5 | 115489 | 2 | AC117072 |
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| c | 386 | 22 | 1.5 | 123508 | 2 | AC127040 |
| | 387 | 22 | 1.5 | 123946 | 9 | AC016648 |
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| c | 407 | 22 | 1.5 | 140115 | 2 | AC091470 |
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AC129755 Rattus no
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AC091426 Mus muscu
AC097039 Rattus no
AC094545 Rattus no
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AL117350 Human DNA
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Continuation (9 of
Continuation (12 o
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AC026432 Homo sapi
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Z83851 Human DNA s
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AC103393 Mus muscu
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AC084024 Homo sapi
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AC087220 Oryza sat
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AC111472 Rattus no
AC124351 Mus muscu
AC118772 Rattus no
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AP003239 Oryza sat
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AC096792 Rattus no
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AC084765 Oryza sat
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AC008334 Drosophil
AC094142 Rattus no
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AC104607 Drosophil

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| c | 473 | 22 | 1.5 | 170848 | 2 | AC106386 |
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| c | 475 | 22 | 1.5 | 171457 | 2 | AC112568 |
| c | 476 | 22 | 1.5 | 172155 | 9 | AC018653 |
| c | 477 | 22 | 1.5 | 172393 | 2 | AC025740 |
| | 478 | 22 | 1.5 | 172662 | 2 | AC121792 |
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| c | 482 | 22 | 1.5 | 173149 | 2 | AL391218 |
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| c | 484 | 22 | 1.5 | 173341 | 2 | AL772202 |
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| | 486 | 22 | 1.5 | 174299 | 2 | AC126429 |
| | 487 | 22 | 1.5 | 174997 | 2 | AC095128 |
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| | 489 | 22 | 1.5 | 175648 | 2 | AC097220 |
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| | 491 | 22 | 1.5 | 175996 | 2 | AC128056 |
| | 492 | 22 | 1.5 | 176036 | 2 | AC128107 |
| c | 493 | 22 | 1.5 | 176037 | 2 | AC127746 |
| | 494 | 22 | 1.5 | 177013 | 2 | AC096176 |
| | 495 | 22 | 1.5 | 177529 | 2 | AC111337 |
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| c | 500 | 22 | 1.5 | 178776 | 2 | AC068217 |
| c | 501 | 22 | 1.5 | 178910 | 2 | AC114434 |
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AC097248 Rattus no
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AC024068 Mus muscu
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AC112163 Mus Muscu
AC096525 Rattus no
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AC121910 Mus muscu
AC117816 Mus muscu
AC126988 Rattus no
AC093994 Rattus no
AC119054 Rattus no
AC102520 Mus muscu
AC115891 Mus muscu
AC055771 Homo sapi
AC112425 Rattus no
AC108318 Rattus no
AC106673 Rattus no
AC093797 Homo sapi
AL355094 Human chr
AC121675 Rattus no
AC111289 Rattus no
AC106386 Rattus no
AC118507 Rattus no
AC112568 Rattus no
AC018653 Homo sapi
AC025740 Homo sapi
AC121792 Mus muscu
AC108526 Rattus no
AC120304 Rattus no
AC116139 Mus muscu
AL391218 Homo sapi
AC107691 Mus muscu
AL772202 Homo sapi
AC010214 Drosophil
AC126429 Mus muscu
AC095128 Rattus no
AC095075 Rattus no
AC097220 Rattus no
AC094475 Rattus no
AC128056 Rattus no
AC128107 Rattus no
AC127746 Rattus no
AC096176 Rattus no
AC111337 Rattus no
AC107119 Rattus no
AC114508 Rattus no
AC107052 Homo sapi
AC125603 Homo sapi
AC068217 Homo sapi
AC114434 Rattus no
AC113647 Rattus no
AC113860 Rattus no

| | | | | | | |
|---|---|---|---|---|---|---|
| 504 | 22 | 1.5 | 179586 | 2 | AC121633 | AC121633 Rattus no |
| c 505 | 22 | 1.5 | 180023 | 2 | AC107230 | AC107230 Mus muscu |
| c 506 | 22 | 1.5 | 180076 | 2 | AC112381 | AC112381 Rattus no |
| 507 | 22 | 1.5 | 180316 | 9 | AC007773 | AC007773 Homo sapi |
| 508 | 22 | 1.5 | 180444 | 10 | AL606924 | AL606924 Mouse DNA |
| c 509 | 22 | 1.5 | 180622 | 2 | AC107835 | AC107835 Mus muscu |
| 510 | 22 | 1.5 | 180741 | 2 | AC109530 | AC109530 Rattus no |
| 511 | 22 | 1.5 | 181100 | 2 | AC124060 | AC124060 Homo sapi |
| c 512 | 22 | 1.5 | 181656 | 2 | AC124900 | AC124900 Rattus no |
| 513 | 22 | 1.5 | 182442 | 2 | AC128099 | AC128099 Rattus no |
| 514 | 22 | 1.5 | 182774 | 2 | AC121054 | AC121054 Rattus no |
| c 515 | 22 | 1.5 | 183159 | 2 | AC126504 | AC126504 Rattus no |
| c 516 | 22 | 1.5 | 183378 | 2 | AC102278 | AC102278 Mus muscu |
| c 517 | 22 | 1.5 | 183454 | 2 | AC121423 | AC121423 Rattus no |
| c 518 | 22 | 1.5 | 183583 | 2 | AC131114 | AC131114 Mus muscu |
| c 519 | 22 | 1.5 | 184557 | 2 | AC114452 | AC114452 Rattus no |
| 520 | 22 | 1.5 | 184558 | 2 | AC093978 | AC093978 Rattus no |
| c 521 | 22 | 1.5 | 184703 | 2 | AL773566 | AL773566 Mus muscu |
| c 522 | 22 | 1.5 | 184875 | 9 | AC025898 | AC025898 Homo sapi |
| c 523 | 22 | 1.5 | 184983 | 9 | HS139I22 | AL136504 Homo sapi |
| c 524 | 22 | 1.5 | 185122 | 2 | AC111761 | AC111761 Rattus no |
| c 525 | 22 | 1.5 | 185393 | 2 | AC116479 | AC116479 Mus muscu |
| 526 | 22 | 1.5 | 185543 | 2 | AC096178 | AC096178 Rattus no |
| c 527 | 22 | 1.5 | 185605 | 2 | AL772351 | AL772351 Mus muscu |
| c 528 | 22 | 1.5 | 185671 | 2 | AC084376 | AC084376 Homo sapi |
| c 529 | 22 | 1.5 | 185800 | 2 | AC079366 | AC079366 Mus muscu |
| c 530 | 22 | 1.5 | 186103 | 2 | AC122593 | AC122593 Rattus no |
| c 531 | 22 | 1.5 | 186144 | 2 | AC091359 | AC091359 Rattus no |
| 532 | 22 | 1.5 | 186390 | 3 | AC007852 | AC007852 Drosophil |
| c 533 | 22 | 1.5 | 186408 | 2 | AC130390 | AC130390 Drosophil |
| c 534 | 22 | 1.5 | 186564 | 2 | AC117184 | AC117184 Mus muscu |
| c 535 | 22 | 1.5 | 186665 | 2 | AC127171 | AC127171 Mus muscu |
| c 536 | 22 | 1.5 | 186760 | 2 | AC126996 | AC126996 Rattus no |
| 537 | 22 | 1.5 | 186762 | 2 | AC126318 | AC126318 Rattus no |
| 538 | 22 | 1.5 | 186766 | 2 | AC096895 | AC096895 Rattus no |
| c 539 | 22 | 1.5 | 186766 | 2 | AC096895 | AC096895 Rattus no |
| c 540 | 22 | 1.5 | 186795 | 2 | AC101776 | AC101776 Mus muscu |
| 541 | 22 | 1.5 | 187196 | 10 | AF520420 | AF520420 Mus muscu |
| 542 | 22 | 1.5 | 188635 | 2 | AC104892 | AC104892 Mus muscu |
| c 543 | 22 | 1.5 | 188981 | 2 | AL772215 | AL772215 Mus muscu |
| c 544 | 22 | 1.5 | 189062 | 2 | AC098444 | AC098444 Rattus no |
| 545 | 22 | 1.5 | 189175 | 2 | AC121200 | AC121200 Rattus no |
| 546 | 22 | 1.5 | 189873 | 2 | AC125736 | AC125736 Rattus no |
| 547 | 22 | 1.5 | 189874 | 2 | AC125155 | AC125155 Mus muscu |
| 548 | 22 | 1.5 | 190174 | 2 | AC111348 | AC111348 Rattus no |
| 549 | 22 | 1.5 | 190180 | 2 | AC110539 | AC110539 Mus muscu |
| c 550 | 22 | 1.5 | 190289 | 10 | AL732540 | AL732540 Mouse DNA |
| c 551 | 22 | 1.5 | 190543 | 2 | AC097794 | AC097794 Rattus no |
| c 552 | 22 | 1.5 | 190598 | 2 | AC126839 | AC126839 Rattus no |
| c 553 | 22 | 1.5 | 190748 | 2 | AC120812 | AC120812 Rattus no |
| c 554 | 22 | 1.5 | 191466 | 3 | AC008348 | AC008348 Drosophil |
| 555 | 22 | 1.5 | 191815 | 2 | AC097557 | AC097557 Rattus no |
| c 556 | 22 | 1.5 | 192362 | 10 | AC068906 | AC068906 Mus muscu |
| 557 | 22 | 1.5 | 192777 | 2 | AC095271 | AC095271 Rattus no |
| 558 | 22 | 1.5 | 192864 | 2 | AC040981 | AC040981 Mus muscu |
| c 559 | 22 | 1.5 | 193283 | 2 | AL844214 | AL844214 Mus muscu |
| c 560 | 22 | 1.5 | 193425 | 9 | AC055733 | AC055733 Homo sapi |
| 561 | 22 | 1.5 | 193495 | 2 | AC108780 | AC108780 Mus muscu |
| 562 | 22 | 1.5 | 193855 | 2 | AC119829 | AC119829 Mus muscu |
| c 563 | 22 | 1.5 | 194439 | 2 | AC122447 | AC122447 Mus muscu |
| c 564 | 22 | 1.5 | 194873 | 2 | AC123465 | AC123465 Rattus no |
| 565 | 22 | 1.5 | 195196 | 2 | AC112465 | AC112465 Rattus no |
| 566 | 22 | 1.5 | 195479 | 2 | AC126660 | AC126660 Rattus no |
| c 567 | 22 | 1.5 | 196664 | 2 | AC131185 | AC131185 Mus muscu |
| 568 | 22 | 1.5 | 196890 | 2 | AC131140 | AC131140 Rattus no |
| c 569 | 22 | 1.5 | 197078 | 2 | AL845536 | AL845536 Mus muscu |
| 570 | 22 | 1.5 | 199306 | 2 | AC068459 | AC068459 Mus muscu |
| 571 | 22 | 1.5 | 199414 | 2 | AC102664 | AC102664 Mus muscu |
| c 572 | 22 | 1.5 | 199555 | 2 | AC115748 | AC115748 Mus muscu |
| 573 | 22 | 1.5 | 199793 | 2 | AC107564 | AC107564 Rattus no |
| 574 | 22 | 1.5 | 199841 | 2 | AC099729 | AC099729 Mus muscu |
| c 575 | 22 | 1.5 | 200822 | 9 | AL591806 | AL591806 Human DNA |
| c 576 | 22 | 1.5 | 200934 | 2 | AC123819 | AC123819 Mus muscu |
| c 577 | 22 | 1.5 | 200995 | 2 | AC123490 | AC123490 Rattus no |
| 578 | 22 | 1.5 | 201618 | 2 | AC117688 | AC117688 Mus muscu |
| 579 | 22 | 1.5 | 203586 | 2 | AC103939 | AC103939 Mus muscu |
| 580 | 22 | 1.5 | 203693 | 2 | AC115278 | AC115278 Rattus no |
| c 581 | 22 | 1.5 | 204394 | 9 | AL590128 | AL590128 Human DNA |
| c 582 | 22 | 1.5 | 204834 | 2 | AL670851 | AL670851 Mus muscu |
| c 583 | 22 | 1.5 | 206082 | 2 | AC126936 | AC126936 Mus muscu |
| c 584 | 22 | 1.5 | 206312 | 2 | AC092725 | AC092725 Homo sapi |
| 585 | 22 | 1.5 | 206600 | 2 | AC116179 | AC116179 Mus muscu |
| 586 | 22 | 1.5 | 206647 | 9 | AP002898 | AP002898 Homo sapi |
| c 587 | 22 | 1.5 | 210636 | 9 | AC006443 | AC006443 Homo sapi |
| 588 | 22 | 1.5 | 210989 | 2 | AL844147 | AL844147 Mus muscu |
| c 589 | 22 | 1.5 | 211221 | 2 | AL807745 | AL807745 Mus muscu |
| 590 | 22 | 1.5 | 211577 | 2 | AL845283 | AL845283 Mus muscu |
| 591 | 22 | 1.5 | 212475 | 2 | AC093021 | AC093021 Mus muscu |
| 592 | 22 | 1.5 | 213547 | 2 | AC106780 | AC106780 Homo sapi |
| 593 | 22 | 1.5 | 214161 | 2 | AC109231 | AC109231 Mus muscu |
| c 594 | 22 | 1.5 | 214216 | 2 | AC026609 | AC026609 Homo sapi |
| c 595 | 22 | 1.5 | 214311 | 2 | AC110576 | AC110576 Mus muscu |
| 596 | 22 | 1.5 | 214870 | 10 | AL606496 | AL606496 Mouse DNA |
| c 597 | 22 | 1.5 | 214897 | 2 | AL805900 | AL805900 Mus muscu |
| c 598 | 22 | 1.5 | 215196 | 2 | AC073796 | AC073796 Mus muscu |
| c 599 | 22 | 1.5 | 216623 | 2 | AC122039 | AC122039 Mus muscu |
| 600 | 22 | 1.5 | 216698 | 2 | AC092006 | AC092006 Bos tauru |
| c 601 | 22 | 1.5 | 216814 | 2 | AC125076 | AC125076 Mus muscu |
| 602 | 22 | 1.5 | 216943 | 2 | AC111914 | AC111914 Rattus no |
| 603 | 22 | 1.5 | 217103 | 2 | AC101774 | AC101774 Mus muscu |
| c 604 | 22 | 1.5 | 217399 | 2 | AL844212 | AL844212 Mus muscu |
| 605 | 22 | 1.5 | 218904 | 2 | AL844840 | AL844840 Mus muscu |
| 606 | 22 | 1.5 | 219148 | 2 | AL806510 | AL806510 Mus muscu |
| c 607 | 22 | 1.5 | 219179 | 2 | AC100600 | AC100600 Mus muscu |
| 608 | 22 | 1.5 | 219751 | 2 | AL732595 | AL732595 Mus muscu |
| 609 | 22 | 1.5 | 221049 | 2 | AL691421 | AL691421 Mus muscu |
| 610 | 22 | 1.5 | 222185 | 2 | AC127697 | AC127697 Mus muscu |
| 611 | 22 | 1.5 | 223326 | 2 | AC127567 | AC127567 Mus muscu |
| 612 | 22 | 1.5 | 223650 | 2 | AC109625 | AC109625 Mus muscu |
| c 613 | 22 | 1.5 | 224227 | 2 | AC104225 | AC104225 Mus muscu |
| c 614 | 22 | 1.5 | 224641 | 2 | AC102505 | AC102505 Mus muscu |
| c 615 | 22 | 1.5 | 224790 | 2 | AC127556 | AC127556 Mus muscu |
| c 616 | 22 | 1.5 | 225448 | 2 | AC122296 | AC122296 Mus muscu |
| 617 | 22 | 1.5 | 226155 | 2 | AC079441 | AC079441 Mus muscu |
| 618 | 22 | 1.5 | 226208 | 2 | AC107712 | AC107712 Mus muscu |
| 619 | 22 | 1.5 | 226594 | 10 | AC087216 | AC087216 Mus muscu |
| c 620 | 22 | 1.5 | 227736 | 2 | AC121825 | AC121825 Mus muscu |
| c 621 | 22 | 1.5 | 227769 | 10 | AC034109 | AC034109 Mus muscu |
| 622 | 22 | 1.5 | 228371 | 10 | AC107317 | AC107317 Mus muscu |
| 623 | 22 | 1.5 | 228780 | 2 | AC123807 | AC123807 Mus muscu |
| c 624 | 22 | 1.5 | 230041 | 2 | AC098522 | AC098522 Rattus no |
| c 625 | 22 | 1.5 | 230591 | 2 | AL772270 | AL772270 Mus muscu |
| 626 | 22 | 1.5 | 230740 | 2 | AC094558 | AC094558 Rattus no |
| 627 | 22 | 1.5 | 231675 | 10 | AL591410 | AL591410 Mouse DNA |
| c 628 | 22 | 1.5 | 232960 | 2 | AC094849 | AC094849 Rattus no |
| c 629 | 22 | 1.5 | 233428 | 2 | AC011064 | AC011064 Drosophil |
| c 630 | 22 | 1.5 | 237232 | 2 | AC122315 | AC122315 Mus muscu |
| 631 | 22 | 1.5 | 237933 | 2 | AC124713 | AC124713 Mus muscu |
| c 632 | 22 | 1.5 | 238551 | 2 | AC095726 | AC095726 Rattus no |
| c 633 | 22 | 1.5 | 240999 | 2 | AC109256 | AC109256 Mus muscu |
| 634 | 22 | 1.5 | 242694 | 2 | AC115360 | AC115360 Mus muscu |
| 635 | 22 | 1.5 | 242804 | 10 | AC024069 | AC024069 Mus muscu |
| c 636 | 22 | 1.5 | 249403 | 2 | AC123072 | AC123072 Mus muscu |
| c 637 | 22 | 1.5 | 251773 | 2 | AC079129 | AC079129 Mus muscu |
| 638 | 22 | 1.5 | 253648 | 3 | AE003638 | AE003638 Drosophil |
| c 639 | 22 | 1.5 | 259575 | 2 | AC126259 | AC126259 Mus muscu |
| 640 | 22 | 1.5 | 264315 | 2 | AC124584 | AC124584 Mus muscu |
| c 641 | 22 | 1.5 | 268819 | 2 | AC103281 | AC103281 Rattus no |
| c 642 | 22 | 1.5 | 280343 | 2 | AC105850 | AC105850 Rattus no |
| c 643 | 22 | 1.5 | 287344 | 3 | AE003816 | AE003816 Drosophil |
| c 644 | 22 | 1.5 | 288411 | 3 | AE003456 | AE003456 Drosophil |
| 645 | 22 | 1.5 | 302672 | 3 | AE003497 | AE003497 Drosophil |
| 646 | 22 | 1.5 | 305346 | 2 | AC125327 | AC125327 Mus muscu |
| 647 | 22 | 1.5 | 310364 | 3 | AE003448 | AE003448 Drosophil |
| 648 | 22 | 1.5 | 318503 | 2 | AC074166 | AC074166 Mus muscu |
| c 649 | 22 | 1.5 | 325791 | 6 | AX234657 | AX234657 Sequence |

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 650 | 21 | 1.4 | 21 | 6 | AX018854 Sequence |
| | 651 | 21 | 1.4 | 35 | 6 | AX052997 Sequence |
| | 652 | 21 | 1.4 | 45 | 6 | AX009974 Sequence |
| c | 653 | 21 | 1.4 | 50 | 6 | I08559 Sequence 1 |
| | 654 | 21 | 1.4 | 51 | 6 | AR182640 Sequence |
| | 655 | 21 | 1.4 | 51 | 6 | AR182643 Sequence |
| c | 656 | 21 | 1.4 | 51 | 6 | AX411413 Sequence |
| c | 657 | 21 | 1.4 | 54 | 6 | AX286167 Sequence |
| c | 658 | 21 | 1.4 | 59 | 6 | AR172678 Sequence |
| c | 659 | 21 | 1.4 | 59 | 6 | AX464846 Sequence |
| | 660 | 21 | 1.4 | 63 | 6 | E26793 Novel prote |
| c | 661 | 21 | 1.4 | 70 | 6 | AX052986 Sequence |
| c | 662 | 21 | 1.4 | 84 | 6 | AX052985 Sequence |
| c | 663 | 21 | 1.4 | 96 | 6 | AX052995 Sequence |
| c | 664 | 21 | 1.4 | 120 | 6 | AX052988 Sequence |
| c | 665 | 21 | 1.4 | 120 | 9 | U00924 Human clone |
| c | 666 | 21 | 1.4 | 121 | 6 | AX324611 Sequence |
| | 667 | 21 | 1.4 | 121 | 6 | AX324612 Sequence |
| c | 668 | 21 | 1.4 | 121 | 6 | AX324615 Sequence |
| | 669 | 21 | 1.4 | 121 | 6 | AX324616 Sequence |
| c | 670 | 21 | 1.4 | 123 | 6 | AX052999 Sequence |
| | 671 | 21 | 1.4 | 130 | 11 | G18911 BMS1522 cow |
| c | 672 | 21 | 1.4 | 155 | 11 | G19041 cow STS BMS |
| | 673 | 21 | 1.4 | 160 | 11 | G19037 cow STS BMS |
| | 674 | 21 | 1.4 | 165 | 10 | MMCOL18A04 Mus musculu |
| | 675 | 21 | 1.4 | 168 | 11 | G19050 cow STS BMS |
| | 676 | 21 | 1.4 | 169 | 11 | G19046 cow STS BMS |
| c | 677 | 21 | 1.4 | 178 | 11 | G19038 cow STS BMS |
| c | 678 | 21 | 1.4 | 182 | 11 | HS349XF5 Z67102 H.sapiens D |
| | 679 | 21 | 1.4 | 186 | 11 | G19039 cow STS BMS |
| | 680 | 21 | 1.4 | 195 | 11 | AF224988 AF224988 Sus scrof |
| c | 681 | 21 | 1.4 | 203 | 9 | HSPRA46 X13471 Human PreA4 |
| | 682 | 21 | 1.4 | 203 | 11 | G19042 G19042 cow STS BMS |
| c | 683 | 21 | 1.4 | 227 | 8 | AY022626 AY022626 Oryza sat |
| | 684 | 21 | 1.4 | 227 | 8 | AY023308 AY023308 Oryza sat |
| | 685 | 21 | 1.4 | 227 | 8 | AY023550 AY023550 Oryza sat |
| c | 686 | 21 | 1.4 | 239 | 8 | AY022630 AY022630 Oryza sat |
| c | 687 | 21 | 1.4 | 281 | 5 | GGRE16G6 X78625 G.gallus ge |
| c | 688 | 21 | 1.4 | 284 | 11 | AU048798 AU048798 Rattus no |
| | 689 | 21 | 1.4 | 285 | 9 | AB03799S02 AB037999 Homo sapi |
| | 690 | 21 | 1.4 | 302 | 3 | AF247461 AF247461 Coptoterm |
| c | 691 | 21 | 1.4 | 311 | 9 | HS198TA1 Z16847 H. sapiens |
| | 692 | 21 | 1.4 | 329 | 6 | A45359 A45359 Sequence 29 |
| | 693 | 21 | 1.4 | 329 | 6 | AR061164 AR061164 Sequence |
| | 694 | 21 | 1.4 | 329 | 9 | HSSRRAA X73214 H.sapiens s |
| c | 695 | 21 | 1.4 | 332 | 8 | AF440265 AF440265 Pinus tae |
| | 696 | 21 | 1.4 | 413 | 5 | HAR403998 AJ403998 Hyla arbo |
| | 697 | 21 | 1.4 | 415 | 11 | AB054754 AB054754 Rattus no |
| | 698 | 21 | 1.4 | 429 | 11 | AU027638 AU027638 Rattus no |
| c | 699 | 21 | 1.4 | 436 | 5 | AF520874 AF520874 Aphelocom |
| | 700 | 21 | 1.4 | 448 | 6 | AX014498 AX014498 Sequence |
| | 701 | 21 | 1.4 | 448 | 6 | E64922 E64922 cDNA sequen |
| | 702 | 21 | 1.4 | 449 | 9 | AB018500 AB018500 Homo sapi |
| | 703 | 21 | 1.4 | 485 | 8 | AB031227 AB031227 Pisum sat |
| | 704 | 21 | 1.4 | 505 | 4 | AF203646 AF203646 Myotis my |
| | 705 | 21 | 1.4 | 505 | 4 | AF203647 AF203647 Myotis my |
| c | 706 | 21 | 1.4 | 531 | 9 | AB018518 AB018518 Homo sapi |
| | 707 | 21 | 1.4 | 532 | 11 | AU029103 AU029103 Rattus no |
| | 708 | 21 | 1.4 | 541 | 9 | AB018497 AB018497 Homo sapi |
| | 709 | 21 | 1.4 | 546 | 11 | AU048021 AU048021 Rattus no |
| c | 710 | 21 | 1.4 | 551 | 8 | AF396032 AF396032 Magnaport |
| | 711 | 21 | 1.4 | 572 | 5 | HAR403997 AJ403997 Hyla arbo |
| | 712 | 21 | 1.4 | 672 | 6 | A39468 A39468 Sequence 1 |
| c | 713 | 21 | 1.4 | 672 | 11 | G10522 G10522 human STS C |
| | 714 | 21 | 1.4 | 673 | 9 | AB018517 AB018517 Homo sapi |
| | 715 | 21 | 1.4 | 673 | 9 | AF329211 AF329211 Homo sapi |
| | 716 | 21 | 1.4 | 680 | 3 | DD5SRNA X67782 D.discoideu |
| | 717 | 21 | 1.4 | 700 | 6 | AR181325 AR181325 Sequence |
| c | 718 | 21 | 1.4 | 737 | 10 | AY055471 AY055471 Mus muscu |
| c | 719 | 21 | 1.4 | 745 | 9 | HUMAMYB06 M34867 Human amylo |
| c | 720 | 21 | 1.4 | 791 | 10 | AF349733 AF349733 Mus muscu |
| c | 721 | 21 | 1.4 | 845 | 9 | HSU06680 U06680 Human clone |
| c | 722 | 21 | 1.4 | 851 | 10 | AF189709 AF189709 Rattus no |
| c | 723 | 21 | 1.4 | 895 | 6 | E02401 E02401 DNA encodin |
| c | 724 | 21 | 1.4 | 909 | 5 | AF262935 AF262935 Gallus ga |
| c | 725 | 21 | 1.4 | 1028 | 9 | AB01755S08 AB017561 Homo sapi |
| | 726 | 21 | 1.4 | 1047 | 11 | G15745 G15745 human STS C |
| c | 727 | 21 | 1.4 | 1086 | 8 | AF322129 AF322129 Cymbopogo |
| c | 728 | 21 | 1.4 | 1113 | 8 | PHVHRGPA M18093 P.vulgaris |
| c | 729 | 21 | 1.4 | 1132 | 9 | AF053478 AF053478 Homo sapi |
| | 730 | 21 | 1.4 | 1186 | 3 | DWU51067 U51067 Drosophila |
| | 731 | 21 | 1.4 | 1195 | 3 | DWU51065 U51065 Drosophila |
| | 732 | 21 | 1.4 | 1198 | 3 | DWU51060 U51060 Drosophila |
| | 733 | 21 | 1.4 | 1198 | 3 | DWU51063 U51063 Drosophila |
| | 734 | 21 | 1.4 | 1198 | 3 | DWU51064 U51064 Drosophila |
| | 735 | 21 | 1.4 | 1201 | 3 | DWU51061 U51061 Drosophila |
| | 736 | 21 | 1.4 | 1201 | 3 | DWU51062 U51062 Drosophila |
| | 737 | 21 | 1.4 | 1201 | 3 | DWU51066 U51066 Drosophila |
| | 738 | 21 | 1.4 | 1204 | 3 | DWU51068 U51068 Drosophila |
| | 739 | 21 | 1.4 | 1207 | 3 | DWU51058 U51058 Drosophila |
| | 740 | 21 | 1.4 | 1207 | 3 | DWU51059 U51059 Drosophila |
| c | 741 | 21 | 1.4 | 1245 | 8 | MZEAGAMOU L81162 Zea maize A |
| c | 742 | 21 | 1.4 | 1308 | 6 | AX488960 AX488960 Sequence |
| c | 743 | 21 | 1.4 | 1319 | 9 | BC004369 BC004369 Homo sapi |
| | 744 | 21 | 1.4 | 1353 | 9 | AF052091 AF052091 Homo sapi |
| c | 745 | 21 | 1.4 | 1413 | 6 | AX375966 AX375966 Sequence |
| c | 746 | 21 | 1.4 | 1444 | 3 | DMDUNC23 X55163 D.melanogas |
| c | 747 | 21 | 1.4 | 1556 | 3 | DMIPOU X58436 D.melanogas |
| c | 748 | 21 | 1.4 | 1566 | 10 | RATMECP2A M94064 Rat MeCP-2 |
| c | 749 | 21 | 1.4 | 1618 | 8 | AY059827 AY059827 Arabidops |
| | 750 | 21 | 1.4 | 1704 | 9 | AF001095 AF001095 Homo sapi |
| | 751 | 21 | 1.4 | 1776 | 6 | AX027881 AX027881 Sequence |
| | 752 | 21 | 1.4 | 1815 | 9 | HSA420897 AJ420897 Homo sapi |
| | 753 | 21 | 1.4 | 1832 | 9 | AF208289 AF208289 Homo sapi |
| c | 754 | 21 | 1.4 | 1845 | 9 | HUMAPP M28373 Homo sapien |
| c | 755 | 21 | 1.4 | 1853 | 5 | CHKNFKB2 D13721 Chicken mRN |
| c | 756 | 21 | 1.4 | 1862 | 6 | AX399846 AX399846 Sequence |
| c | 757 | 21 | 1.4 | 1880 | 3 | LCSHEATH2 Z35443 Litomosoide |
| c | 758 | 21 | 1.4 | 1925 | 8 | AY054679 AY054679 Arabidops |
| | 759 | 21 | 1.4 | 1956 | 9 | HSU32248 U32248 Human mRNA |
| c | 760 | 21 | 1.4 | 2019 | 10 | MMMMP9B X72795 M.musculus |
| c | 761 | 21 | 1.4 | 2052 | 9 | AF217977 AF217977 Homo sapi |
| c | 762 | 21 | 1.4 | 2080 | 3 | AF086816 AF086816 Drosophil |
| c | 763 | 21 | 1.4 | 2085 | 6 | I29797 I29797 Sequence 9 |
| c | 764 | 21 | 1.4 | 2088 | 6 | A33292 A33292 H.sapiens A |
| c | 765 | 21 | 1.4 | 2088 | 6 | AX105391 AX105391 Sequence |
| c | 766 | 21 | 1.4 | 2088 | 6 | AX105393 AX105393 Sequence |
| c | 767 | 21 | 1.4 | 2088 | 6 | AX105395 AX105395 Sequence |
| c | 768 | 21 | 1.4 | 2094 | 6 | AX105397 AX105397 Sequence |
| c | 769 | 21 | 1.4 | 2094 | 6 | AX105399 AX105399 Sequence |
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| | 771 | 21 | 1.4 | 2107 | 10 | MMA2APLAS Y12312 M.musculus |
| c | 772 | 21 | 1.4 | 2120 | 8 | ATAACPTA Z36910 A.thaliana |
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| c | 774 | 21 | 1.4 | 2253 | 6 | AX105438 AX105438 Sequence |
| c | 775 | 21 | 1.4 | 2256 | 6 | AR072105 AR072105 Sequence |
| c | 776 | 21 | 1.4 | 2256 | 6 | I06116 I06116 Sequence 6 |
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| | 780 | 21 | 1.4 | 2263 | 3 | LMU29952 U29952 Leishmania |
| c | 781 | 21 | 1.4 | 2265 | 6 | A33293 A33293 H.sapiens A |
| c | 782 | 21 | 1.4 | 2265 | 6 | AX002735 AX002735 Sequence |
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| c | 785 | 21 | 1.4 | 2310 | 6 | AX348248 AX348248 Sequence |
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| c | 788 | 21 | 1.4 | 2316 | 6 | AX105440 AX105440 Sequence |
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| c | 790 | 21 | 1.4 | 2360 | 6 | E02400 E02400 DNA encodin |
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| c 797 | 21 | 1.4 | 2681 | 8 | CAL320271 | AJ320271 Candida a |
| c 798 | 21 | 1.4 | 2735 | 6 | AX286180 | AX286180 Sequence |
| c 799 | 21 | 1.4 | 2855 | 8 | NCU17641 | U17641 Neurospora |
| c 800 | 21 | 1.4 | 3006 | 10 | BC024690 | BC024690 Mus muscu |
| c 801 | 21 | 1.4 | 3012 | 6 | AX286173 | AX286173 Sequence |
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| c 803 | 21 | 1.4 | 3092 | 6 | AR180971 | AR180971 Sequence |
| c 804 | 21 | 1.4 | 3148 | 6 | I36122 | I36122 Sequence 3 |
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| c 806 | 21 | 1.4 | 3160 | 10 | MUSGEL | D12712 Mouse mRNA |
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| c 808 | 21 | 1.4 | 3196 | 10 | S67830 | S67830 type IV col |
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| 828 | 21 | 1.4 | 4343 | 2 | AC014123 | AC014123 Drosophil |
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| c 830 | 21 | 1.4 | 4844 | 8 | AF170083 | AF170083 Candida a |
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| c 832 | 21 | 1.4 | 4906 | 3 | AY075346 | AY075346 Drosophil |
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| 840 | 21 | 1.4 | 5634 | 10 | AF353728S2 | AF353729 Mus muscu |
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| c 845 | 21 | 1.4 | 6769 | 9 | AB011151 | AB011151 Homo sapi |
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| c 847 | 21 | 1.4 | 6868 | 6 | AX229858 | AX229858 Sequence |
| c 848 | 21 | 1.4 | 6916 | 6 | AX026121 | AX026121 Sequence |
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| c 850 | 21 | 1.4 | 7382 | 3 | DROGLDGMCA | M29299 Drosophila |
| 851 | 21 | 1.4 | 7601 | 10 | RATALGL | M24108 Rattus norv |
| c 852 | 21 | 1.4 | 7838 | 10 | MMU428065 | AJ428065 Mus muscu |
| 853 | 21 | 1.4 | 8127 | 2 | AC012916 | AC012916 Drosophil |
| c 854 | 21 | 1.4 | 8190 | 10 | MMMMP9A | X72794 M.musculus |
| c 855 | 21 | 1.4 | 8372 | 10 | AF216218 | AF216218 Rattus no |
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| c 857 | 21 | 1.4 | 8591 | 6 | I58322 | I58322 Sequence 6 |
| c 858 | 21 | 1.4 | 8591 | 6 | I58323 | I58323 Sequence 8 |
| c 859 | 21 | 1.4 | 8591 | 6 | I60508 | I60508 Sequence 6 |
| c 860 | 21 | 1.4 | 8591 | 6 | I60509 | I60509 Sequence 8 |
| c 861 | 21 | 1.4 | 8591 | 6 | I77052 | I77052 Sequence 6 |
| c 862 | 21 | 1.4 | 8591 | 6 | I77053 | I77053 Sequence 8 |
| c 863 | 21 | 1.4 | 8591 | 6 | I87173 | I87173 Sequence 6 |
| c 864 | 21 | 1.4 | 8591 | 6 | I87174 | I87174 Sequence 8 |
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| 866 | 21 | 1.4 | 10108 | 9 | HUMHOXRAGE | D28769 Human HOX12 |
| 867 | 21 | 1.4 | 10716 | 9 | HSM736A3A | AL049708 Human DNA |
| 868 | 21 | 1.4 | 11052 | 6 | AX348372 | AX348372 Sequence |
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| c 870 | 21 | 1.4 | 11664 | 10 | S78114 | S78114 Mus musculu |
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| c 887 | 21 | 1.4 | 24001 | 9 | AC012385 | AC012385 Homo sapi |
| c 888 | 21 | 1.4 | 25812 | 2 | AC017367 | AC017367 Drosophil |
| c 889 | 21 | 1.4 | 27785 | 2 | AC116978 | AC116978 Dictyoste |
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| c 896 | 21 | 1.4 | 32096 | 3 | CEF21A3 | Z81509 Caenorhabdi |
| 897 | 21 | 1.4 | 32746 | 2 | AC013224 | AC013224 Drosophil |
| 898 | 21 | 1.4 | 33673 | 3 | AC006672 | AC006672 Caenorhab |
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| c 900 | 21 | 1.4 | 34033 | 2 | AC017819 | AC017819 Drosophil |
| 901 | 21 | 1.4 | 34283 | 3 | AC036105 | AC036105 Leishmani |
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| 904 | 21 | 1.4 | 36328 | 3 | LMFL5213 | AL583932 Leishmani |
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| 906 | 21 | 1.4 | 37762 | 3 | AC005836 | AC005836 Leishmani |
| 907 | 21 | 1.4 | 39425 | 3 | AC009601 | AC009601 Leishmani |
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| 912 | 21 | 1.4 | 41737 | 2 | AC115866 | AC115866 Mus muscu |
| c 913 | 21 | 1.4 | 44640 | 2 | AC130957 | AC130957 Rattus no |
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| c 916 | 21 | 1.4 | 45761 | 2 | AC116959 | AC116959 Dictyoste |
| 917 | 21 | 1.4 | 46960 | 2 | AC117300 | AC117300 Rattus no |
| c 918 | 21 | 1.4 | 47544 | 2 | AC123636 | AC123636 Mus muscu |
| 919 | 21 | 1.4 | 47563 | 2 | AC017461 | AC017461 Drosophil |
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| c 921 | 21 | 1.4 | 48504 | 2 | AC017427 | AC017427 Drosophil |
| c 922 | 21 | 1.4 | 48504 | 4 | AL731846 | AL731846 Sminthops |
| 923 | 21 | 1.4 | 50572 | 2 | AC023899 | AC023899 Mus muscu |
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| 974 | 21 | 1.4 | 67659 | 2 | AC118689 | AC118689 Mus muscu |
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| c 979 | 21 | 1.4 | 68478 | 8 | NCB12F1 | AL390091 Neurospor |
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| c 997 | 21 | 1.4 | 72822 | 2 | AC126786 | AC126786 Medicago |
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ALIGNMENTS

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RESULT 1
AX018850
LOCUS       AX018850               1493 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9943800.
ACCESSION   AX018850
VERSION     AX018850.1  GI:10042952
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1493)
  AUTHORS   Durrant,L.G. and Spendlove,I.
  TITLE     Tumor associated antigen 791tgp72
  JOURNAL   Patent: WO 9943800-A 5 02-SEP-1999;
            DURRANT LINDA GILLIAN (GB); SPENDLOVE IAN (GB); CANCER RES CAMPAIGN
            TECH (GB)
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
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BASE COUNT      401 a    355 c    355 g    382 t
ORIGIN
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Query Match 100.0%; Score 1493; DB 6; Length 1493;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1493; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 GTCGTGCATGTGGTGGTGGTGGTGGTGGTTAACCATGGTGGCGGGCCGCCACTGTGCTGG 120
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Qy     121 ATATCTGCAGAATTCGATGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTT 180
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Db     181 GTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTC 240

Qy     241 CTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGT 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGT 300

Qy     301 GACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGT 360
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Db     301 GACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGT 360

Qy     361 TTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGC 420

Qy     421 GAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 GAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGC 480

Qy     481 AATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATC 540

Qy     541 ACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGA 600

Qy     601 AGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCA 660
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Db    601 AGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCA 660

Qy    661 GTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATT 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATT 720

Qy    721 GATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTAC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTAC 780

Qy    781 AAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGT 840

Qy    841 GACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGA 900
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Db    841 GACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGA 900

Qy    901 ATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAAT 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAAT 960

Qy    961 AAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGA 1020

Qy   1021 GAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCA 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCA 1080

Qy   1081 ACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAG 1140
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Db   1081 ACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAG 1140

Qy   1141 AAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCC 1200
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Db   1141 AAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCC 1200

Qy   1201 AGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGT 1260
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Db   1201 AGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGT 1260

Qy   1261 ACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTA 1320
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Db   1261 ACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTA 1320

Qy   1321 GTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTAT 1380
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Db   1321 GTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTAT 1380

Qy   1381 ACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTG 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 ACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTG 1440

Qy   1441 CTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db   1441 CTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493


RESULT 2
AX018846
LOCUS       AX018846               2102 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 1 from Patent WO9943800.
ACCESSION   AX018846
VERSION     AX018846.1  GI:10042948
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2102)
  AUTHORS   Durrant,L.G. and Spendlove,I.
  TITLE     Tumor associated antigen 791tgp72
  JOURNAL   Patent: WO 9943800-A 1 02-SEP-1999;
            DURRANT LINDA GILLIAN (GB); SPENDLOVE IAN (GB); CANCER RES CAMPAIGN
            TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .2102
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC07712.1"
                     /db_xref="GI:10042949"
                     /translation="MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPN
                     AQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPT
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
BASE COUNT      661 a    419 c    445 g    577 t
ORIGIN

  Query Match             90.8%;  Score 1356;  DB 6;  Length 2102;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
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Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724
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Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Db     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
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Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
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Db    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy    1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy    1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
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Db    1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy    1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
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Db    1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy    1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db    1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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RESULT 3
AX333057
LOCUS       AX333057               2102 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3566 from Patent WO0194629.
ACCESSION   AX333057
VERSION     AX333057.1  GI:18123691
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3566 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .2102
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      661 a    419 c    445 g    577 t
ORIGIN

  Query Match             90.8%;  Score 1356;  DB 6;  Length 2102;
  Best Local Similarity   100.0%;  Pred. No. 0;
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  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
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Db      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
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Db     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
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Db     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
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Db     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
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Db     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
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Db     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
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Db     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Db     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Qy     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
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Db     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
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Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084
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Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
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Db   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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Db   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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RESULT 4
HUMDAFB
LOCUS       HUMDAFB                 2102 bp    mRNA    linear   PRI 02-NOV-1994
DEFINITION  Human decay-accelerating factor mRNA, complete cds.
ACCESSION   M31516
VERSION     M31516.1  GI:181467
KEYWORDS    alternative splicing; decay-accelerating factor; membrane
            glycoprotein.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2102)
  AUTHORS   Caras,I.W., Davitz,M.A., Rhee,L., Weddell,G., Martin,D.W. Jr. and
            Nussenzweig,V.
  TITLE     Cloning of decay-accelerating factor suggests novel use of splicing
            to generate two proteins
  JOURNAL   Nature 325 (6104), 545-549 (1987)
  MEDLINE   87115845
   PUBMED   2433596
COMMENT     The gene for decay accelerating factor produces two proteins by
            alternative splicing.  The spliced out region is between positions
            1147 and 1148.
FEATURES             Location/Qualifiers
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
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                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
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                     /note="G00-119-088; putative"
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BASE COUNT      661 a    419 c    445 g    577 t
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Query Match 90.8%; Score 1356; DB 9; Length 2102;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
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RESULT 5
I05091
LOCUS       I05091                  2115 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 2 from Patent EP 0244267.
ACCESSION   I05091
VERSION     I05091.1  GI:591251
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2115)
  AUTHORS   Caras,I.W.
  TITLE     Variants of decay accelerating factor (DAF) prepared by recombinant
            DNA technology
  JOURNAL   Patent: EP 0244267-A2 2 04-NOV-1987;
FEATURES             Location/Qualifiers
     source          1. .2115
                     /organism="unknown"
BASE COUNT      675 a    419 c    445 g    576 t
ORIGIN

  Query Match             90.8%;  Score 1356;  DB 6;  Length 2115;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 6
I09215
LOCUS       I09215                  2115 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8901041.
ACCESSION   I09215
VERSION     I09215.1  GI:588075
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2115)
  AUTHORS   Caras,I.W.
  TITLE     NUCLEIC ACID AND METHODS FOR THE SYNTHESIS OF NOVEL FUSION
            POLYPEPTIDES WITH A PHOSPHOLIPID ANCHOR DOMAIN
  JOURNAL   Patent: WO 8901041-A 1 09-FEB-1989;
FEATURES             Location/Qualifiers
     source          1. .2115
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BASE COUNT      675 a    419 c    446 g    575 t
ORIGIN

  Query Match             90.8%;  Score 1356;  DB 6;  Length 2115;
  Best Local Similarity   100.0%;  Pred. No. 0;
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Qy     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
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Qy     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
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Db     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
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Db     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

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Db     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy    1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
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Db    1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204

Qy    1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
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Db    1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264

Qy    1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324

Qy    1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
           |||||||||||||||||||||||||||||||||||
Db    1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360


RESULT 7
BC001288
LOCUS       BC001288                1357 bp    mRNA    linear   PRI 12-JUL-2001
DEFINITION  Homo sapiens, Similar to decay accelerating factor for complement
            (CD55, Cromer blood group system), clone MGC:5192 IMAGE:3460621,
            mRNA, complete cds.
ACCESSION   BC001288
VERSION     BC001288.1  GI:12654888
KEYWORDS    MGC.
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SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1357)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2000) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 4 Row: d Column: 2
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 181467.
FEATURES              Location/Qualifiers
     source           1. .1357
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                      /db_xref="taxon:9606"
                      /clone="MGC:5192 IMAGE:3460621"
                      /tissue_type="Cervix, carcinoma"
                      /clone_lib="NIH_MGC_12"
                      /lab_host="DH10B"
                      /note="Vector: pCMV-SPORT6"
     CDS              80. .1225
                      /codon_start=1
                      /product="Similar to decay accelerating factor for
                      complement (CD55, Cromer blood group system)"
                      /protein_id="AAH01288.1"
                      /db_xref="GI:12654889"
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                      KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                      ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                      SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                      RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
BASE COUNT      401 a    325 c    304 g    327 t
ORIGIN
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  Query Match             87.7%;  Score 1310;  DB 9;  Length 1357;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
Db     19 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC  78

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
Db     79 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 138

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
Db    139 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 198

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
Db    199 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 258

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
Db    259 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 318

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
Db    319 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 378

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
Db    379 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 438

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
Db    439 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 498

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
Db    499 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 558

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
Db    559 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 618

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
Db    619 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 678

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
Db    679 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 738

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
Db    739 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 798

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
Db    799 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 858

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
Db    859 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 918

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
Db    919 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 978

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
Db    979 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1038

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
Db   1039 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1098

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
Db   1099 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1158

Qy   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337
Db   1159 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1218

Qy   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397
Db   1219 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1278

Qy   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCA 1447
Db   1279 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCA 1328
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RESULT 8
AX202076
LOCUS       AX202076               2263 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 6 from Patent WO0153531.
ACCESSION   AX202076
VERSION     AX202076.1  GI:15391861
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2263)
  AUTHORS   Phippard,D., Vasanthakamur,G., Dotson,S. and Ma,X.J.
  TITLE     Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
            and cells
  JOURNAL   Patent: WO 0153531-A 6 26-JUL-2001;
            Pharmacia Corporation (US)
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     source          1. .2263
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BASE COUNT      706 a    475 c    474 g    607 t      1 others
ORIGIN

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  Matches 1346;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    148 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 207
Db    161 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 220

Qy    208 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 267
Db    221 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 280

Qy    268 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 327
Db    281 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 340

Qy    328 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 387
Db    341 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 400

Qy    388 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 447
Db    401 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 460

Qy    448 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 507
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Qy    508 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 567
Db    521 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 580

Qy    568 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 627
Db    581 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 640

Qy    628 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 687
Db    641 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 700

Qy    688 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 747
Db    701 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 760

Qy    748 GCAACCAT-CTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 806
Db    761 GCAACCATGCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 820

Qy    807 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 866
Db    821 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 880

Qy    867 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 926
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Qy    927 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 986
Db    941 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 1000

Qy    987 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1046
Db   1001 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1060

Qy   1047 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1106
Db   1061 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1120

Qy   1107 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1166
Db   1121 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1180

Qy   1167 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1226
Db   1181 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1240

Qy   1227 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1286
Db   1241 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1300

Qy   1287 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1346
Db   1301 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1360

Qy   1347 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1406
Db   1361 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1420

Qy   1407 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1466
Db   1421 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1480

Qy   1467 CTTTAAGATGTGTTAGGAATGTCAACA 1493
Db   1481 CTTTAAGATGTGTTAGGAATGTCAACA 1507


RESULT 9
I41330
LOCUS       I41330                 2096 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5624837.
ACCESSION   I41330
VERSION     I41330.1  GI:2081920
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2096)
  AUTHORS   Fodor,W.L., Rollins,S. and Squinto,S.P.
  TITLE     Nucleic acid encoding chimeric complement inhibitor proteins
  JOURNAL   Patent: US 5624837-A 1 29-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .2096
                     /organism="unknown"
BASE COUNT      671 a    416 c    439 g    570 t
ORIGIN

  Query Match           80.0%;  Score 1195;  DB 6;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
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Qy    146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
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Db      1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy    206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy    266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
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Db    121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy    326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
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Db    181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy    386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy    566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
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Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685
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Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985
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Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy   1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy   1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
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Qy   1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
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Db   1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy   1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
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Db   1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy   1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
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Db   1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy   1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy   1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
          ||||||||||||||||||||||||||||
Db   1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
```

RESULT 10
I49078

```
LOCUS       I49078                  2096 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5627264.
ACCESSION   I49078
VERSION     I49078.1  GI:2467541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2096)
  AUTHORS   Fodor,W.L., Rollins,S. and Squinto,S.P.
  TITLE     Chimeric complement inhibitor proteins
  JOURNAL   Patent: US 5627264-A 1 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .2096
                     /organism="unknown"
BASE COUNT      671 a    416 c    439 g    570 t
ORIGIN
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Query Match 80.0%; Score 1195; DB 6; Length 2096;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1345; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy    206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy    266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy    326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy    386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy    566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625
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Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685

Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745

Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805

Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865

Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925

Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985

Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045

Db    841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy   1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105

Db    901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy   1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165

Db    961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy   1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225

Db   1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy   1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285

Db   1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy   1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345

Db   1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy   1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405

Db   1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy   1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465

Db   1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy   1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493

Db   1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348


RESULT 11
I50941
LOCUS       I50941                 2096 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 10 from patent US 5643770.
ACCESSION   I50941
VERSION     I50941.1  GI:2472644
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2096)
  AUTHORS   Mason,J.M. and Squinto,S.P.
  TITLE     Retroviral vector particles expressing complement inhibitor
            activity
  JOURNAL   Patent: US 5643770-A 10 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .2096
                     /organism="unknown"
BASE COUNT      671 a    416 c    439 g    570 t
ORIGIN

  Query Match             80.0%;  Score 1195;  DB 6;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1345;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    146 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 205

Db      1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy    206 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 265

Db     61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy    266 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 325

Db    121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy    326 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 385

Db    181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy    386 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 445

Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    446 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 505

Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    506 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 565

Db    361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy    566 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 625

Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    626 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 685

Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    686 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 745

Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    746 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 805

Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    806 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 865

Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    866 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 925

Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    926 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 985

Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    986 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 1045
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Db        841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy       1046 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy       1106 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy       1166 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy       1226 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy       1286 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy       1346 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy       1406 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy       1466 TCTTTAAGATGTGTTAGGAATGTCAACA 1493
              ||||||||||||||||||||||||||||
Db       1321 TCTTTAAGATGTGTTAGGAATGTCAACA 1348
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RESULT 12
HUMDAFA
LOCUS       HUMDAFA                 2220 bp    mRNA    linear   PRI 02-NOV-1994
DEFINITION  Human decay-accelerating factor mRNA, complete cds.
ACCESSION   M30142
VERSION     M30142.1  GI:181464
KEYWORDS    Alu repeat; alternative splicing; decay-accelerating factor;
            membrane glycoprotein.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2220)
  AUTHORS   Caras,I.W., Davitz,M.A., Rhee,L., Weddell,G., Martin,D.W. Jr. and
            Nussenzweig,V.
  TITLE     Cloning of decay-accelerating factor suggests novel use of splicing
            to generate two proteins
  JOURNAL   Nature 325 (6104), 545-549 (1987)
  MEDLINE   87115845
   PUBMED   2433596
COMMENT     The gene for decay accelerating factor produces two proteins by
            alternative splicing.  The spliced out region is from position
            1147-1265.  The stop codon in this case is located at position
            1327-1329.  Though mRNAs do not have introns, the alternative
            coding region is indicated in the features table.
FEATURES             Location/Qualifiers
     source          1. .2220
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="1q32"
                     /cell_line="HeLa"
     mRNA            <1. .2220
                     /gene="DAF"
                     /note="G00-119-088"
     gene            join(66. .1146,1265. .1329)
                     /gene="DAF"
     CDS             join(66. .1146,1265. .1329)
                     /gene="DAF"
                     /codon_start=1
                     /product="decay-accelerating factor A"
                     /protein_id="AAA52168.1"
                     /db_xref="GI:181465"
                     /db_xref="GDB:G00-119-088"
                     /translation="MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPN
                     AQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPT
                     RLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKK
                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
     sig_peptide     66. .167
                     /gene="DAF"
                     /note="G00-119-088"
     mat_peptide     join(168. .1146,1265. .1326)
                     /gene="DAF"
                     /product="decay-accelerating factor A"
                     /note="G00-119-088"
     exon            <66. .1146
                     /gene="DAF"
                     /note="decay-accelerating factor precursor A"
                     /number=1
     mat_peptide     168. .1385
                     /gene="DAF"
                     /product="decay-accelerating factor A"
                     /note="G00-119-088"
     intron          1147. .1264
                     /gene="DAF"
                     /note="G00-119-088"
     repeat_region   1150. .1264
                     /note="Alu repeat (partial)"
     exon            1265. .>1329
                     /gene="DAF"
                     /note="G00-119-088"
                     /number=2
     polyA_signal    1410. .1415
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1693. .1698
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1731. .1736
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    2198. .2203
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_site      2220
                     /gene="DAF"
                     /note="G00-119-088"
BASE COUNT       681 a     455 c     475 g     609 t
ORIGIN

  Query Match             76.6%;  Score 1143;  DB 9;  Length 2220;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy        198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy        258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy        318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTCCCGAGGATACTGT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
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Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGG 1280
          |||
Db   1145 TGG 1147


RESULT 13
I09216
LOCUS       I09216                  2233 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 3 from Patent WO 8901041.
ACCESSION   I09216
VERSION     I09216.1  GI:588076
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2233)
  AUTHORS   Caras,I.W.
  TITLE     NUCLEIC ACID AND METHODS FOR THE SYNTHESIS OF NOVEL FUSION
            POLYPEPTIDES WITH A PHOSPHOLIPID ANCHOR DOMAIN
  JOURNAL   Patent: WO 8901041-A 3 09-FEB-1989;
FEATURES             Location/Qualifiers
     source          1. .2233
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BASE COUNT      695 a    455 c    475 g    608 t
ORIGIN

  Query Match           76.6%;  Score 1143;  DB 6;  Length 2233;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1143;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64

Qy    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124

Qy    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184

Qy    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244

Qy    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304

Qy    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364

Qy    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424

Qy    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484

Qy    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544

Qy    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604

Qy    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664

Qy    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724

Qy    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784

Qy    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Db    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844

Qy    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904

Qy   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964

Qy   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024

Qy   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084

Qy   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144

Qy   1278 TGG 1280
          |||
Db   1145 TGG 1147


RESULT 14
HUMDAF
LOCUS       HUMDAF                  2017 bp    mRNA    linear   PRI 02-NOV-1994
DEFINITION  Human complement decay-accelerating factor (DAF) mRNA; 3' end.
ACCESSION   M15799
VERSION     M15799.1  GI:181462
KEYWORDS    complement decay-accelerating factor.
SOURCE      Human HeLa cell cDNA to mRNA, clones DF1 and DF2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2017)
  AUTHORS   Medof,M.E., Lublin,D.M., Holers,V.M., Ayers,D.J., Getty,R.R.,
            Leykam,J.F., Atkinson,J.P. and Tykocinski,M.L.
  TITLE     Cloning and characterization of cDNAs encoding the complete
            sequence of decay-accelerating factor of human complement
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (7), 2007-2011 (1987)
  MEDLINE   87175602
   PUBMED   2436222
COMMENT     Draft entry and computer-readable sequence [1] kindly provided by
            M.L.Tykocinski, 24-OCT-1988.
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                     /note="decay-accelerating factor precursor"
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                     PGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREI
                     YCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPP
                     ECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKH
                     FHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
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                     /note="decay-accelerating factor signal peptide"
     mat_peptide     88. .1128
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BASE COUNT      654 a    390 c    414 g    559 t
ORIGIN      186 bp upstream of HindIII site.

  Query Match             75.5%;  Score 1127;  DB 9;  Length 2017;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1277;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy    214 CCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTG 273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTG 60

Qy    274 CTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCC 333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCC 120

Qy    334 CAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGT 393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGT 180

Qy    394 GAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGT 453
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    181 GAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTAAGGGCATG 240

Qy    454 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 300

Qy    514 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 360

Qy    574 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 420

Qy    634 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 480

Qy    694 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 540

Qy    754 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 600

Qy    814 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 660

Qy    874 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 933
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Db    661 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 720

Qy    934 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 993
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Db    721 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 780

Qy    994 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 1053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 840

Qy   1054 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 900

Qy   1114 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 1173
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Db    901 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 960

Qy   1174 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1233
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1020

Qy   1234 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC 1293
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC 1080

Qy   1294 ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAG 1353
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAG 1140

Qy   1354 AGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGC 1413
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGC 1200

Qy   1414 ATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAG 1473
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAG 1260

Qy   1474 ATGTGTTAGGAATGTCAACA 1493
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Db    1261 ATGTGTTAGGAATGTCAACA 1280


RESULT 15
A65264
LOCUS       A65264                 2237 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 1 from Patent WO9735886.
ACCESSION   A65264
VERSION     A65264.1  GI:4531048
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2237)
  AUTHORS   Watkins,N.J.
  TITLE     SURFACES WHICH PREVENT OR REDUCE COMPLEMENT ACTIVATION
  JOURNAL   Patent: WO 9735886-A 1 02-OCT-1997;
            IMUTRAN LTD (GB)
COMMENT     Other publication AU 1933897 19971017.
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BASE COUNT      699 a    456 c    474 g    608 t
ORIGIN

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Qy    184 CTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTC 243
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Qy    244 GGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGAC 303
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Qy    304 TGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTT 363
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Qy    364 CCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG 423
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    424 AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAAT 483
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Qy    484 CGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACT 543
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Db    350 CGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACT 409

Qy    544 CAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGA 603
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Qy    604 GAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTC 663
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Qy    904 ATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAA 963
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Qy    964 GGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAG 1023
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Db    830 GGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAG 889

Qy   1024 TGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACA 1083
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Qy   1084 GTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAA 1143
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Qy   1144 ACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGG 1203
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Qy   1204 ACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACT 1263
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Search completed: February 24, 2003, 05:25:34
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Job time : 3920.53 secs

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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 02:00:57 ; Search time 3053.89 Seconds
(without alignments)
11147.382 Million cell updates/sec

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Perfect score: 2102
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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3: em_estin:*
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21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
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| | 4 | 842 | 40.1 | 1003 | 9 | AL542661 | AL542661 AL542661 |
| | 5 | 782 | 37.2 | 927 | 9 | AL543593 | AL543593 AL543593 |
| | 6 | 751 | 35.7 | 1025 | 14 | BM806293 | BM806293 AGENCOURT |
| | 7 | 746 | 35.5 | 1073 | 14 | BQ051183 | BQ051183 AGENCOURT |
| | 8 | 744 | 35.4 | 912 | 14 | BQ216954 | BQ216954 AGENCOURT |
| | 9 | 737 | 35.1 | 1079 | 13 | BM544653 | BM544653 AGENCOURT |
| | 10 | 724 | 34.4 | 916 | 14 | BQ221490 | BQ221490 AGENCOURT |
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| | 12 | 719 | 34.2 | 901 | 14 | BQ221579 | BQ221579 AGENCOURT |
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| | 15 | 707 | 33.6 | 849 | 9 | AL541069 | AL541069 AL541069 |
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| | 20 | 670 | 31.9 | 895 | 14 | BQ230137 | BQ230137 AGENCOURT |
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| | 24 | 660 | 31.4 | 945 | 14 | BQ233015 | BQ233015 AGENCOURT |
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| | 26 | 652 | 31.0 | 942 | 14 | BQ436298 | BQ436298 AGENCOURT |
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| c | 28 | 644 | 30.6 | 644 | 10 | AW850641 | AW850641 IL3-CT021 |
| | 29 | 642 | 30.5 | 861 | 14 | BQ231176 | BQ231176 AGENCOURT |
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| | 63 | 550 | 26.2 | 558 | 14 | BM854824 | BM854824 K-EST0137 |
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| | 85 | 505 | 24.0 | 866 | 12 | BG622131 |
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| c | 104 | 480 | 22.8 | 677 | 10 | AW473772 |
| | 105 | 475 | 22.6 | 1054 | 14 | BM925410 |
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| | 107 | 473 | 22.5 | 671 | 12 | BG612173 |
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| c 550 | 22 | 1.0 | 573 | 10 | BE592954 | BE592954 WS1_92_E0 |
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| 562 | 22 | 1.0 | 945 | 17 | CNS013O1 | AL103099 Drosophil |
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| c 571 | 21 | 1.0 | 240 | 9 | AU074448 | AU074448 AU074448 |
| c 572 | 21 | 1.0 | 257 | 14 | W84098 | W84098 T2918 MVAT4 |
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| 586 | 21 | 1.0 | 351 | 9 | AA319511 | AA319511 EST21747 |
| 587 | 21 | 1.0 | 355 | 17 | AA550620 | AA550620 1799m3 gm |
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| | 672 | 21 | 1.0 | 716 | 17 | AG121140 AG121140 Pan trogl |
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| | 697 | 21 | 1.0 | 1812 | 12 | BF128319 BF128319 601810118 |
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| | 713 | 20 | 1.0 | 287 | 10 | BB346148 BB346148 BB346148 |
| | 714 | 20 | 1.0 | 288 | 9 | AI565318 AI565318 ti73a05.x |
| c | 715 | 20 | 1.0 | 300 | 14 | C31899 C31899 C31899 Yuji |
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| c | 719 | 20 | 1.0 | 316 | 14 | D71871 D71871 CELK083A1R |
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| | 731 | 20 | 1.0 | 364 | 9 | AU164087 AU164087 AU164087 |
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| | 745 | 20 | 1.0 | 419 | 13 | BJ411547 BJ411547 BJ411547 |
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| | 748 | 20 | 1.0 | 425 | 17 | AZ977100 AZ977100 2M0252E19 |
| | 749 | 20 | 1.0 | 428 | 13 | BI811596 BI811596 S006B05 O |
| | 750 | 20 | 1.0 | 428 | 17 | AZ720360 AZ720360 RPCI-24-9 |
| c | 751 | 20 | 1.0 | 429 | 12 | BF424932 BF424932 su52g10.y |
| c | 752 | 20 | 1.0 | 435 | 9 | AI732013 AI732013 BNLGHi140 |
| | 753 | 20 | 1.0 | 435 | 14 | BQ791266 BQ791266 E4142 Chi |
| c | 754 | 20 | 1.0 | 437 | 9 | AI731985 AI731985 BNLGHi104 |
| c | 755 | 20 | 1.0 | 438 | 9 | AI732024 AI732024 BNLGHi639 |
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| | 757 | 20 | 1.0 | 440 | 13 | BI807144 BI807144 S084F01 S |
| c | 758 | 20 | 1.0 | 442 | 12 | BG047528 BG047528 saa72c12. |
| c | 759 | 20 | 1.0 | 445 | 17 | AZ467922 AZ467922 1M0279F08 |
| | 760 | 20 | 1.0 | 448 | 12 | BG551318 BG551318 sad36c06. |
| | 761 | 20 | 1.0 | 448 | 17 | BH202590 BH202590 Sm1-56G11 |
| | 762 | 20 | 1.0 | 450 | 17 | AQ503722 AQ503722 RPCI-11-2 |
| c | 763 | 20 | 1.0 | 451 | 12 | BF405957 BF405957 UI-R-CA1- |
| | 764 | 20 | 1.0 | 453 | 9 | AA127271 AA127271 zn89e12.s |
| | 765 | 20 | 1.0 | 457 | 12 | BF355409 BF355409 CM1-HT084 |
| c | 766 | 20 | 1.0 | 457 | 17 | AQ224355 AQ224355 HS_2258_B |
| | 767 | 20 | 1.0 | 459 | 9 | AU172487 AU172487 AU172487 |
| | 768 | 20 | 1.0 | 460 | 9 | AU100848 AU100848 AU100848 |
| c | 769 | 20 | 1.0 | 461 | 13 | BM634492 BM634492 170006875 |
| c | 770 | 20 | 1.0 | 463 | 12 | BF399950 BF399950 UI-R-CA1- |
| | 771 | 20 | 1.0 | 464 | 12 | BG046959 BG046959 saa75a05. |
| | 772 | 20 | 1.0 | 470 | 10 | BE215373 BE215373 HV_CEb000 |
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| | 774 | 20 | 1.0 | 476 | 9 | AA004974 AA004974 zh94c02.r |
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| | 777 | 20 | 1.0 | 479 | 13 | BM276330 BM276330 PfESToaa8 |
| | 778 | 20 | 1.0 | 482 | 17 | AZ296623 AZ296623 RPCI-23-1 |
| c | 779 | 20 | 1.0 | 484 | 17 | AZ013541 AZ013541 RPCI-23-2 |
| c | 780 | 20 | 1.0 | 487 | 9 | AA141298 AA141298 CK01525.5 |
| | 781 | 20 | 1.0 | 495 | 17 | BH384492 BH384492 AG-ND-130 |
| c | 782 | 20 | 1.0 | 500 | 12 | BG305404 BG305404 fm12h12.x |
| c | 783 | 20 | 1.0 | 504 | 12 | BG318685 BG318685 NXPV_017_ |
| | 784 | 20 | 1.0 | 508 | 12 | BF624032 BF624032 HVSMEa000 |
| | 785 | 20 | 1.0 | 509 | 10 | AW890764 AW890764 MR0-NT005 |
| c | 786 | 20 | 1.0 | 510 | 12 | BF717587 BF717587 fd47c05.y |
| c | 787 | 20 | 1.0 | 510 | 13 | BI362461 BI362461 RE47020.5 |
| c | 788 | 20 | 1.0 | 516 | 13 | BI235744 BI235744 RE31665.5 |
| | 789 | 20 | 1.0 | 517 | 13 | BI798190 BI798190 H100C06 E |
| c | 790 | 20 | 1.0 | 517 | 17 | BH215286 BH215286 1006026C1 |
| | 791 | 20 | 1.0 | 518 | 17 | TA69C12Q AL458487 T. brucei |
| | 792 | 20 | 1.0 | 520 | 14 | BQ739636 BQ739636 PfESToab4 |
| | 793 | 20 | 1.0 | 523 | 9 | AL793235 AL793235 AL793235 |
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| | 795 | 20 | 1.0 | 526 | 13 | BI807295 BI807295 S092H09 S |
| | 796 | 20 | 1.0 | 527 | 10 | AW762271 AW762271 ur55g12.y |
| c | 797 | 20 | 1.0 | 527 | 13 | BI634542 BI634542 RH38722.5 |
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| c | 801 | 20 | 1.0 | 533 | 17 | AZ389163 AZ389163 1M0149J24 |
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| c | 804 | 20 | 1.0 | 542 | 17 | TA37C06Q AL455361 T. brucei |
| | 805 | 20 | 1.0 | 544 | 13 | BI804866 BI804866 S001D02 S |
| c | 806 | 20 | 1.0 | 544 | 17 | AZ580599 AZ580599 1M0368K24 |
| c | 807 | 20 | 1.0 | 547 | 13 | BI605065 BI605065 RH70581.5 |
| c | 808 | 20 | 1.0 | 548 | 13 | BI581635 BI581635 RH19162.5 |
| | 809 | 20 | 1.0 | 550 | 13 | BI810646 BI810646 K002H09 O |

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| | 810 | 20 | 1.0 | 553 | 12 | BF127585 BF127585 601810235 |
| c | 811 | 20 | 1.0 | 554 | 12 | BF717800 BF717800 fd51h12.y |
| c | 812 | 20 | 1.0 | 554 | 12 | BG235841 BG235841 EtESTed15 |
| | 813 | 20 | 1.0 | 559 | 13 | BI804891 BI804891 S001G01 S |
| c | 814 | 20 | 1.0 | 561 | 9 | AI542509 AI542509 SD08853.5 |
| | 815 | 20 | 1.0 | 561 | 13 | BI805759 BI805759 S047D02 S |
| | 816 | 20 | 1.0 | 563 | 13 | BI806446 BI806446 S063E01 S |
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| | 818 | 20 | 1.0 | 566 | 17 | AZ635961 AZ635961 1M0493D02 |
| | 819 | 20 | 1.0 | 570 | 10 | AW410748 AW410748 fh08b08.x |
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| | 821 | 20 | 1.0 | 570 | 14 | BQ260493 BQ260493 fz70e01.x |
| c | 822 | 20 | 1.0 | 571 | 17 | AQ702627 AQ702627 HS_5421_B |
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| | 827 | 20 | 1.0 | 584 | 12 | BG106652 BG106652 602290481 |
| c | 828 | 20 | 1.0 | 586 | 9 | AI239069 AI239069 GH15241.5 |
| | 829 | 20 | 1.0 | 587 | 10 | BE581204 BE581204 kq43f03.y |
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| c | 831 | 20 | 1.0 | 596 | 12 | BG495832 BG495832 602540220 |
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| | 833 | 20 | 1.0 | 602 | 14 | BQ908506 BQ908506 T009D09 O |
| c | 834 | 20 | 1.0 | 606 | 13 | BI483297 BI483297 RE66169.5 |
| c | 835 | 20 | 1.0 | 607 | 13 | BI503083 BI503083 BB170008B |
| | 836 | 20 | 1.0 | 608 | 9 | AL661310 AL661310 AL661310 |
| | 837 | 20 | 1.0 | 609 | 17 | BH693294 BH693294 BOMHI42TR |
| | 838 | 20 | 1.0 | 610 | 10 | BE313942 BE313942 601147350 |
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| c | 845 | 20 | 1.0 | 622 | 14 | BQ413786 BQ413786 GA__Ed007 |
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| | 847 | 20 | 1.0 | 625 | 13 | BM037873 BM037873 S113d09 S |
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| | 857 | 20 | 1.0 | 639 | 17 | AQ653720 AQ653720 Sheared D |
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| | 860 | 20 | 1.0 | 647 | 17 | AG060416 AG060416 Pan trogl |
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| c | 862 | 20 | 1.0 | 654 | 13 | BI237730 BI237730 RE34015.5 |
| c | 863 | 20 | 1.0 | 656 | 14 | BP028230 BP028230 BP028230 |
| | 864 | 20 | 1.0 | 660 | 13 | BJ034953 BJ034953 BJ034953 |
| c | 865 | 20 | 1.0 | 666 | 13 | BM168045 BM168045 EST570568 |
| c | 866 | 20 | 1.0 | 668 | 13 | BI509596 BI509596 BB170019A |
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| c | 869 | 20 | 1.0 | 676 | 17 | AG065117 AG065117 Pan trogl |
| | 870 | 20 | 1.0 | 680 | 13 | BJ345456 BJ345456 BJ345456 |
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| c | 872 | 20 | 1.0 | 681 | 13 | BM586261 BM586261 170006873 |
| | 873 | 20 | 1.0 | 687 | 17 | AG103127 AG103127 Pan trogl |
| c | 874 | 20 | 1.0 | 691 | 17 | AG183415 AG183415 Pan trogl |
| c | 875 | 20 | 1.0 | 694 | 9 | AI239043 AI239043 GH15213.5 |
| | 876 | 20 | 1.0 | 698 | 17 | AQ944396 AQ944396 Sheared D |
| c | 877 | 20 | 1.0 | 703 | 13 | BI234734 BI234734 RE30482.5 |
| | 878 | 20 | 1.0 | 711 | 12 | BF214276 BF214276 601848474 |
| c | 879 | 20 | 1.0 | 717 | 13 | BJ051324 BJ051324 BJ051324 |
| | 880 | 20 | 1.0 | 719 | 17 | AZ313123 AZ313123 1M0029P18 |
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| c | 882 | 20 | 1.0 | 724 | 12 | BG290185 BG290185 602385273 |
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| | 885 | 20 | 1.0 | 749 | 10 | BE295311 BE295311 601175804 |
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| | 887 | 20 | 1.0 | 769 | 17 | AG182065 AG182065 Pan trogl |
| | 888 | 20 | 1.0 | 770 | 12 | BF306028 BF306028 601893735 |
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| | 890 | 20 | 1.0 | 805 | 9 | AJ395203 AJ395203 AJ395203 |
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| c | 893 | 20 | 1.0 | 851 | 17 | BH237269 BH237269 AUIIB66TR |
| c | 894 | 20 | 1.0 | 857 | 17 | AZ670730 AZ670730 ENTLJ87TR |
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| | 896 | 20 | 1.0 | 861 | 17 | BH133762 BH133762 ENTOW85TR |
| c | 897 | 20 | 1.0 | 862 | 17 | CNS00D7J AL060325 Drosophil |
| | 898 | 20 | 1.0 | 866 | 13 | BI114707 BI114707 602861735 |
| c | 899 | 20 | 1.0 | 868 | 17 | AZ534723 AZ534723 ENTBG01TR |
| | 900 | 20 | 1.0 | 869 | 13 | BI114444 BI114444 602862114 |
| c | 901 | 20 | 1.0 | 874 | 17 | CNS01ODQ AL153390 Anopheles |
| c | 902 | 20 | 1.0 | 878 | 17 | CNS02S1O AL211317 Tetraodon |
| | 903 | 20 | 1.0 | 879 | 12 | BG825558 BG825558 602749774 |
| | 904 | 20 | 1.0 | 879 | 17 | AZ531170 AZ531170 ENTCL38TF |
| | 905 | 20 | 1.0 | 880 | 17 | CNS05PAM AL347719 Tetraodon |
| | 906 | 20 | 1.0 | 883 | 12 | BG178760 BG178760 602328676 |
| | 907 | 20 | 1.0 | 884 | 17 | CNS03VBC AL262209 Tetraodon |
| | 908 | 20 | 1.0 | 897 | 14 | BQ424967 BQ424967 AGENCOURT |
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| | 910 | 20 | 1.0 | 917 | 13 | BM459608 BM459608 AGENCOURT |
| | 911 | 20 | 1.0 | 919 | 17 | BH130910 BH130910 ENTOZ03TR |
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| | 913 | 20 | 1.0 | 930 | 17 | CNS01ZKS AL174421 Tetraodon |
| | 914 | 20 | 1.0 | 931 | 17 | AZ668244 AZ668244 ENTFH06TR |
| | 915 | 20 | 1.0 | 933 | 12 | BG745368 BG745368 602723705 |
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| c | 917 | 20 | 1.0 | 945 | 14 | BQ947563 BQ947563 AGENCOURT |
| | 918 | 20 | 1.0 | 956 | 14 | BQ651466 BQ651466 AGENCOURT |
| | 919 | 20 | 1.0 | 973 | 12 | BE905705 BE905705 601495717 |
| | 920 | 20 | 1.0 | 979 | 17 | CNS0188V AL109033 Drosophil |
| | 921 | 20 | 1.0 | 981 | 13 | BI252000 BI252000 602952641 |
| | 922 | 20 | 1.0 | 988 | 13 | BM561174 BM561174 AGENCOURT |
| c | 923 | 20 | 1.0 | 996 | 17 | CNS00LV1 AL078785 Drosophil |
| c | 924 | 20 | 1.0 | 998 | 17 | CNS044C9 AL273906 Tetraodon |
| c | 925 | 20 | 1.0 | 1004 | 14 | BQ716402 BQ716402 AGENCOURT |
| c | 926 | 20 | 1.0 | 1008 | 17 | CNS0050K AL056575 Drosophil |
| | 927 | 20 | 1.0 | 1014 | 17 | CNS046CW AL276521 Tetraodon |
| | 928 | 20 | 1.0 | 1019 | 13 | BM460975 BM460975 AGENCOURT |
| | 929 | 20 | 1.0 | 1024 | 14 | BQ643964 BQ643964 AGENCOURT |
| | 930 | 20 | 1.0 | 1040 | 17 | CNS00CLR AL059036 Drosophil |
| | 931 | 20 | 1.0 | 1043 | 14 | BQ062308 BQ062308 AGENCOURT |
| | 932 | 20 | 1.0 | 1048 | 14 | BQ058584 BQ058584 AGENCOURT |
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| | 935 | 20 | 1.0 | 1113 | 14 | BQ647840 BQ647840 AGENCOURT |
| | 936 | 20 | 1.0 | 1168 | 14 | BM927616 BM927616 AGENCOURT |
| | 937 | 20 | 1.0 | 1206 | 14 | BQ062399 BQ062399 AGENCOURT |
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| | 941 | 19 | 0.9 | 60 | 12 | BG910593 BG910593 602812625 |
| c | 942 | 19 | 0.9 | 104 | 17 | BH603557 BH603557 BOHLJ67TF |
| | 943 | 19 | 0.9 | 133 | 17 | BH396490 BH396490 AG-ND-119 |
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| | 945 | 19 | 0.9 | 142 | 14 | D19444 D19444 MUSGS00822 |
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| c | 948 | 19 | 0.9 | 158 | 9 | AU014564 AU014564 AU014564 |
| | 949 | 19 | 0.9 | 159 | 9 | AU013422 AU013422 AU013422 |
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| | 951 | 19 | 0.9 | 169 | 9 | AU013436 AU013436 AU013436 |
| c | 952 | 19 | 0.9 | 172 | 17 | AZ458513 AZ458513 1M0262J11 |
| | 953 | 19 | 0.9 | 178 | 9 | AU008292 AU008292 AU008292 |
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| 956 | 19 | 0.9 | 182 | 14 | U31429 | U31429 HSU31429 Hu |
| 957 | 19 | 0.9 | 185 | 9 | AU013609 | AU013609 AU013609 |
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| 959 | 19 | 0.9 | 187 | 17 | BH077544 | BH077544 RPCI-24-3 |
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| 962 | 19 | 0.9 | 190 | 10 | BB488758 | BB488758 BB488758 |
| c 963 | 19 | 0.9 | 192 | 9 | AL372938 | AL372938 MtBA54F04 |
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| 965 | 19 | 0.9 | 194 | 14 | T39363 | T39363 ya04h10.r2 |
| 966 | 19 | 0.9 | 203 | 10 | AW139958 | AW139958 UI-H-BI1- |
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| 968 | 19 | 0.9 | 210 | 17 | BH389668 | BH389668 AG-ND-143 |
| 969 | 19 | 0.9 | 211 | 9 | AU009073 | AU009073 AU009073 |
| 970 | 19 | 0.9 | 211 | 9 | AU009074 | AU009074 AU009074 |
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| 972 | 19 | 0.9 | 211 | 17 | AZ847610 | AZ847610 2M0148F15 |
| 973 | 19 | 0.9 | 214 | 10 | AV358386 | AV358386 AV358386 |
| c 974 | 19 | 0.9 | 214 | 13 | BM127854 | BM127854 if10b09.x |
| c 975 | 19 | 0.9 | 214 | 13 | BM128403 | BM128403 if14a07.x |
| 976 | 19 | 0.9 | 214 | 14 | BQ787120 | BQ787120 il50e02.y |
| c 977 | 19 | 0.9 | 215 | 10 | AW614104 | AW614104 hg75e12.x |
| c 978 | 19 | 0.9 | 215 | 13 | BI357151 | BI357151 RE43543.5 |
| 979 | 19 | 0.9 | 216 | 10 | BB061478 | BB061478 BB061478 |
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| c 981 | 19 | 0.9 | 222 | 14 | D24819 | D24819 RICR2609A R |
| c 982 | 19 | 0.9 | 223 | 9 | AL691826 | AL691826 DKFZp313F |
| 983 | 19 | 0.9 | 224 | 12 | BG259850 | BG259850 602371804 |
| c 984 | 19 | 0.9 | 226 | 17 | AZ837781 | AZ837781 2M0133O11 |
| 985 | 19 | 0.9 | 227 | 10 | BB062808 | BB062808 BB062808 |
| c 986 | 19 | 0.9 | 227 | 13 | BM274293 | BM274293 PfESToaa4 |
| 987 | 19 | 0.9 | 227 | 17 | BH440553 | BH440553 BOHHY63TR |
| c 988 | 19 | 0.9 | 229 | 17 | AZ096004 | AZ096004 RPCI-23-4 |
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| 990 | 19 | 0.9 | 230 | 9 | AV096467 | AV096467 AV096467 |
| c 991 | 19 | 0.9 | 233 | 9 | AU013501 | AU013501 AU013501 |
| c 992 | 19 | 0.9 | 238 | 9 | AI984383 | AI984383 wr88c03.x |
| c 993 | 19 | 0.9 | 238 | 10 | AW003756 | AW003756 ws16e08.x |
| c 994 | 19 | 0.9 | 240 | 9 | AI522147 | AI522147 ti78g02.x |
| c 995 | 19 | 0.9 | 240 | 9 | AI738946 | AI738946 wi12d02.x |
| c 996 | 19 | 0.9 | 240 | 10 | AW006838 | AW006838 ws15a06.x |
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| 1000 | 19 | 0.9 | 244 | 13 | BM128142 | BM128142 if10b09.y |

ALIGNMENTS

RESULT 1
AL550277
LOCUS AL550277 1074 bp mRNA linear EST 16-FEB-2001
DEFINITION AL550277 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI039YF15 5 prime, mRNA sequence.
ACCESSION AL550277
VERSION AL550277.1 GI:12887094
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .1074
/organism="Homo sapiens"
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/clone="CS0DI039YF15"
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/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng.Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 312 a 257 c 238 g 264 t 3 others
ORIGIN

Query Match 45.2%; Score 950; DB 9; Length 1074;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1000; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124
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Db       1 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 60

Qy     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184
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Qy     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364
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Db     241 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 300

Qy     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424
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Db     301 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 360

Qy     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484
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Db     361 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 420

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Qy     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784
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Db     661 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 720

Qy     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844
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Qy     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904
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Qy     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964
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Db     841 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 900

Qy     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024
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Db     901 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 960

Qy    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTT 1065
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Db     961 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTT 1001


RESULT 2
AL547977/c
LOCUS       AL547977               1033 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL547977 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI035YJ20 3
            prime, mRNA sequence.
ACCESSION   AL547977
VERSION     AL547977.1  GI:12882550
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1033)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
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                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      312 a    188 c    159 g    371 t      3 others
ORIGIN

  Query Match           42.1%;  Score 885;  DB 9;  Length 1033;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  935;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy    1174 TGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAA 1233
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Qy    1234 ATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAA 1293
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Qy    1294 TAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAAT 1353
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Db     782 TAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAAT 723

Qy    1354 GTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACC 1413
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Db     722 GTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTAACACACCTACACC 663

Qy    1414 TCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAA 1473
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Qy    1474 GCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGAAAAGAGAAGGAAAGTGATTT 1533
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Db     602 GCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGAAAAGAGAAGGAAAGTGATTT 543

Qy    1534 TTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGGAAATAAAAAATGAAAAACAT 1593
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Db     542 TTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGGAAATAAAAAATGAAAAACAT 483

Qy    1594 TATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCTCTTCTAAGCAAAATTGCTAA 1653
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Db     482 TATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCTCTTCTAAGCAAAATTGCTAA 423

Qy    1654 AGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTC 1713
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Db     422 AGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTC 363

Qy    1714 GGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGGTGTTGATGGTGAT 1773
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Db     362 GGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGGTGTTGATGGTGAT 303

Qy    1774 AAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGTTGCACAAATAGAGTTTGGAA 1833
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Qy    1834 AAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGAGATACTAC 1893
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Db     242 AAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGAGATACTAC 183

Qy    1894 AATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATT 1953
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Db     182 AATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATAGTCAAATT 123

Qy    1954 TGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGA 2013
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Db     122 TGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATTTATGACAGTGAACATTCTGA 63

Qy    2014 TTTTACATGTAAAACAAGAAAAGTTGAAGAAGATAT 2049
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Db      62 TTTTACATGTAAAACAAGAAAAGTTGAAGAAGATAT 27


RESULT 3
AL575907/c
LOCUS       AL575907               1000 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL575907 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI067YL02 3
            prime, mRNA sequence.
ACCESSION   AL575907
VERSION     AL575907.1  GI:12937532
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      249 a    205 c    225 g    319 t      2 others
ORIGIN

  Query Match           41.2%;  Score 866;  DB 9;  Length 1000;
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Db     969 ACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTA 910

Qy     355 GCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGA 414
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Db     909 GCTGCGAGGTGCCAACAAGGCTTAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGA 850

Qy     415 ATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAAC 474
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Db     849 ATTATCTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAAC 790

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Db     789 CTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAAT 730

Qy     535 TTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTAC 594
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Qy     595 CAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTAT 654
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Qy     715 TGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTC 774
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Qy     775 AAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGAT 834
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Db     489 AAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGAT 430

Qy     835 TCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGA 894
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Db     429 TCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGA 370

Qy     895 GTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTC 954
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Qy     955 AGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCA 1014
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Qy    1015 CCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAA 1074
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Qy    1075 CCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCC 1134
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Db     189 CCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCC 130

Qy    1135 GTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCA 1194
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Db     129 GTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCA 70

Qy    1195 TGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACT 1254
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Qy    1255 GTTCCTAG 1262
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RESULT 4
AL542661
LOCUS       AL542661               1003 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL542661 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE014YB04 5 prime
            , mRNA sequence.
ACCESSION   AL542661
VERSION     AL542661.1  GI:12874926
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1003)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      278 a    239 c    233 g    247 t      6 others
ORIGIN

  Query Match           40.1%;  Score 842;  DB 9;  Length 1003;
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  Matches  842;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db       1 GCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCT 60

Qy     119 GCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCT 178
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Db      61 GCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCT 120

Qy     179 TCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGA 238
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Db    121 TCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGA 180

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Qy    299 AGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTG 358
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Db    361 TTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTC 420

Qy    479 TCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTG 538
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Db    421 TCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTG 480

Qy    539 TAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGG 598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGG 540

Qy    599 TGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGG 658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGG 600

Qy    659 CTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCC 718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCC 660

Qy    719 AGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGG 778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGG 720

Qy    779 GGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCAC 838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCAC 780

Qy    839 CATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGG 898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGG 840

Qy    899 CC 900
          ||
Db    841 CC 842


RESULT 5
AL543593
LOCUS       AL543593                927 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL543593 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI006YE18 5
            prime, mRNA sequence.
ACCESSION   AL543593
VERSION     AL543593.1  GI:12876072
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 927)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .927
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI006YE18"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      248 a    217 c    224 g    237 t      1 others
ORIGIN

  Query Match             37.2%;  Score 782;  DB 9;  Length 927;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches  902;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy     40 GCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGC 99
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Db      1 GCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGC 60

Qy    100 TGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCG 159
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Db     61 TGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCG 120

Qy    160 TGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCC 219
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCC 180

Qy    220 GTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAA 279
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAA 240

Qy    280 TTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAG 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAG 300

Qy    340 AGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGC 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGC 360

Qy    400 CTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAG 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAG 420

Qy    460 GTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGT 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGT 480

Qy    520 CCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATG 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATG 540

Qy    580 GTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACA 639
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    541 GTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAA-CATCTCCTTCTCATGTAACA 599

Qy    640 CAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCC 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    600 CAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCC 659

Qy    700 AGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTG 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 AGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTG 719

Qy    760 ACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATG 819
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Db     720 ACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATG 779

Qy     820 CATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATG 879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 CATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATG 839

Qy     880 ATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGG 939
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 ATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGG 899

Qy     940 TCC 942
           |||
Db     900 TCC 902


RESULT 6
BM806293
LOCUS       BM806293                1025 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  AGENCOURT_6542718 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548732
            5', mRNA sequence.
ACCESSION   BM806293
VERSION     BM806293.1  GI:19123116
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1025)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12258  row: c  column: 05
            High quality sequence stop: 713.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5548732"
                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      253 a    260 c    254 g    254 t      4 others
ORIGIN

  Query Match             35.7%;  Score 751;  DB 14;  Length 1025;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  751;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      27 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 86

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      87 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 146

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     147 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 206

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
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Db     207 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 266

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     267 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 326

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     327 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 386

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     387 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 446

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     447 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 506

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     507 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 566

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     567 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 626

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     627 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 686

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     687 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 746

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACC 751
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Db     747 AGTGCAGAGAAATTTATTGTCCAGCACCACC 777


RESULT 7
BQ051183
LOCUS       BQ051183                1073 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6763621 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5792538
            5', mRNA sequence.
ACCESSION   BQ051183
VERSION     BQ051183.1  GI:19810523
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1073)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12891  row: a  column: 19
            High quality sequence stop: 628.
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                     /tissue_type="large cell carcinoma"
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                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      321 a    275 c    227 g    250 t
ORIGIN

  Query Match             35.5%;  Score 746;  DB 14;  Length 1073;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  746;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    285 GGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTC 344
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     12 GGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTC 71

Qy    345 TGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTAT 404
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 TGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTAT 131

Qy    405 ATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC 464
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 ATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTAC 191

Qy    465 AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACA 524
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Db    192 AGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACA 251

Qy    525 GCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAG 584
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 GCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAG 311

Qy    585 ATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGG 644
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 ATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGG 371

Qy    645 TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGG 704
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 TACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGG 431

Qy    705 AGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAAT 764
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 AGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAAT 491

Qy    765 GGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGT 824
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    492 GGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGT 551

Qy    825 AATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAA 884
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Db    552 AATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAA 611

Qy    885 GGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCA 944
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    612 GGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCA 671

Qy    945 CCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCT 1004
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    672 CCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCT 731

Qy   1005 CAGAAAACCACCACAAAAACCACCAC 1030
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Db    732 CAGAAAACCACCACAAAAACCACCAC 757


RESULT 8
BQ216954
LOCUS       BQ216954                912 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7549174 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059366
            5', mRNA sequence.
ACCESSION   BQ216954
VERSION     BQ216954.1  GI:20398354
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13325  row: o  column: 15
            High quality sequence stop: 614.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6059366"
                     /clone_lib="NIH_MGC_68"
                     /tissue_type="large cell carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.8 kb.   Library constructed by Life
                     Technologies. "
BASE COUNT      224 a    218 c    233 g    236 t      1 others
ORIGIN

  Query Match             35.4%;  Score 744;  DB 14;  Length 912;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  744;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      8 GCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCAT 67
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCAT 60

Qy     68 GACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCT 127
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCT 120

Qy    128 GCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGA 187
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGA 180

Qy    188 TGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAAT 247
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAAT 240

Qy    248 AACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTG 307
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTG 300

Qy    308 CCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCC 367
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCC 360

Qy    368 AACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGT 427
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGT 420

Qy    428 CGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACC 487
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACC 480

Qy    488 AAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAA 547
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAA 540

Qy    548 ATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATT 607
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATT 600

Qy    608 ATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTC 667
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTC 660

Qy    668 TAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAG 727
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAG 720

Qy    728 AGAAATTTATTGTCCAGCACCACC 751
          |||||||||||||||||||||||
Db    721 AGAAATTTATTGTCCAGCACCACC 744


RESULT 9
BM544653
LOCUS       BM544653                1079 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6494695 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5727356
            5', mRNA sequence.
ACCESSION   BM544653
VERSION     BM544653.1  GI:18776079
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1079)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12721  row: e  column: 21
            High quality sequence stop: 724.
FEATURES             Location/Qualifiers
     source          1. .1079
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                     /clone="IMAGE:5727356"
                     /clone_lib="NIH_MGC_124"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: EcoRV
                     (destroyed); Site_2: NotI; RNA source male hippocampus,
                     age 27. Library is oligo-dT primed and directionally
                     cloned (EcoRV site is destroyed upon cloning). Average
                     insert size 1.4 kb, insert size range 0.9-4 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 012."
BASE COUNT      286 a    274 c    252 g    265 t      2 others
ORIGIN

  Query Match           35.1%;  Score 737;  DB 13;  Length 1079;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  737;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      25 CGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGA 84
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      47 CGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGA 106

Qy      85 GCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGT 144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107 GCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGT 166

Qy     145 TGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGC 204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     167 TGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGC 226

Qy     205 CAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAG 264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     227 CAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAG 286

Qy     265 AAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAAT 324
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     287 AAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAAT 346

Qy     325 GGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTG 384
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     347 GGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTG 406

Qy     385 CATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAAT 444
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     407 CATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAAT 466

Qy     445 ATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTC 504
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     467 ATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTC 526

Qy     505 AGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGG 564
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     527 AGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGG 586

Qy     565 GAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCT 624
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     587 GAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCT 646

Qy     625 CCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTT 684
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     647 CCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTT 706

Qy     685 CAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAG 744
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     707 CAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAG 766

Qy     745 CACCACCACAAATTGAC 761
           |||||||||||||||||
Db     767 CACCACCACAAATTGAC 783


RESULT 10
BQ221490
LOCUS       BQ221490                916 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7567431 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6060184
            5', mRNA sequence.
ACCESSION   BQ221490
VERSION     BQ221490.1  GI:20402890
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
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            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13328  row: a  column: 17
            High quality sequence stop: 662.
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                      /db_xref="taxon:9606"
                      /clone="IMAGE:6060184"
                      /clone_lib="NIH_MGC_68"
                      /tissue_type="large cell carcinoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.8 kb.   Library constructed by Life
                      Technologies. "
BASE COUNT      236 a    214 c    232 g    234 t
ORIGIN

  Query Match             34.4%;  Score 724;  DB 14;  Length 916;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  724;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      28 AGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCG 87
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCG 60

Qy      88 TGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGT 147
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGT 120

Qy     148 GCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAG 207
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAG 180

Qy     208 CTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAA 267
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAA 240

Qy     268 GCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGT 327
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGT 300

Qy     328 CAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCAT 387
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCAT 360

Qy     388 CCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATG 447
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATG 420

Qy     448 AGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGA 507
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGA 480

Qy     508 ATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAG 567
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAG 540

Qy     568 AAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCT 627
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCT 600

Qy     628 TCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAG 687
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Db     601 TCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAG 660

Qy     688 GCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCAC 747
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 GCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCAC 720

Qy     748 CACC 751
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Db     721 CACC 724


RESULT 11
BQ228452
LOCUS       BQ228452                880 bp    mRNA    linear   EST 02-MAY-2002
DEFINITION  AGENCOURT_7657435 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059688
            5', mRNA sequence.
ACCESSION   BQ228452
VERSION     BQ228452.1  GI:20409852
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13326  row: m  column: 01
            High quality sequence stop: 615.
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                      /clone="IMAGE:6059688"
                      /clone_lib="NIH_MGC_68"
                      /tissue_type="large cell carcinoma"
                      /lab_host="DH10B (phage-resistant)"
                      /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                      Average insert size 1.8 kb.   Library constructed by Life
                      Technologies. "
BASE COUNT      286 a    200 c    175 g    219 t
ORIGIN

  Query Match             34.3%;  Score 720;  DB 14;  Length 880;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  720;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     446 TGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCA 505
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 TGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCA 60

Qy     506 GAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGG 565
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGG 120

Qy     566 AGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTC 625
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTC 180

Qy     626 CTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTC 685
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTC 240

Qy     686 AGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGC 745
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGC 300

Qy     746 ACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACA 805
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATATAGACA 360
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Qy     806 GTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTG 865
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Db     361 GTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTG 420

Qy     866 TACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATC 925
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Db     421 TACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATC 480

Qy     926 TCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTAC 985
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Db     481 TCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTAC 540

Qy     986 AGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGC 1045
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGC 600

Qy    1046 AACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAA 1105
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAA 660

Qy    1106 AGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTT 1165
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Db     661 AGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTT 720
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RESULT 12
BQ221579
LOCUS BQ221579 901 bp mRNA linear EST 02-MAY-2002
DEFINITION AGENCOURT_7549729 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6057673 5', mRNA sequence.
ACCESSION BQ221579
VERSION BQ221579.1 GI:20402979
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 901)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13321 row: i column: 02
High quality sequence stop: 705.
FEATURES Location/Qualifiers
source 1. .901
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6057673"
/clone_lib="NIH_MGC_68"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.8 kb. Library constructed by Life Technologies. "
BASE COUNT 321 a 176 c 171 g 231 t 2 others
ORIGIN

Query Match 34.2%; Score 719; DB 14; Length 901;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 769; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     768 ATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAAT 827
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAAT 60

Qy     828 AAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGA 887
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGA 120

Qy     888 GAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCA 947
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCA 180

Qy     948 ACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAG 1007
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAG 240

Qy    1008 AAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCC 1067
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCC 300

Qy    1068 AGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGT 1127
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Db     301 AGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGT 360

Qy    1128 ACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTA 1187
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Qy    1188 GTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTAT 1247
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Db     421 GTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTAT 480

Qy    1248 ACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTG 1307
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Qy    1308 CTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAG 1367
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Db     541 CTCTTCATTTAGGATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAG 600

Qy    1368 GAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAA 1427
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Db     601 GAGAAAAAAGGCAGTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAA 660

Qy    1428 CAACTTGCAGAATTGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGT 1487
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Db     661 CAACTTGCAGAATTGAGAGTGATTCCTTTCCTANAAGTGTAAGAAAGCATAGAGATTTGT 720

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RESULT 13
BQ051318
LOCUS BQ051318 1016 bp mRNA linear EST 29-MAR-2002
DEFINITION AGENCOURT_6763612 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5792705 5', mRNA sequence.
ACCESSION BQ051318
VERSION BQ051318.1 GI:19810658
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1016)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

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           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM12891  row: h  column: 18
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Qy      63 GCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCC 122
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Qy     363 GTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTT 422
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LOCUS       AL541261                862 bp    mRNA    linear   EST 16-FEB-2001
DEFINITION  AL541261 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005YG14 5 prime
            , mRNA sequence.
ACCESSION   AL541261
VERSION     AL541261.1  GI:12872159
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 862)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                     /lab_host="DH10B"
                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
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ORIGIN

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Qy     195 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 254
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Qy     255 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 314
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Qy     315 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 374
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Qy     375 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 434
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Db    433 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 492

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Qy    555 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTTGGT 614
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Qy    615 GCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTT 674
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Qy    675 TGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATT 734
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Qy    795 GGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGA 850
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Db    792 GGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGA 847
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DEFINITION  AL541069 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005YG07 5 prime
            , mRNA sequence.
ACCESSION   AL541069
VERSION     AL541069.1  GI:12871785
KEYWORDS    EST.
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 849)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                     /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
                     cDNA was primed with a NotI-oligo(dT) primer. Five prime
                     end enriched, double-stranded cDNA was digested with Not I
                     and cloned into the Not I and Eco RV sites of the
                     pCMVSPORT 6 vector.  Library was constructed by Life
                     Technologies. Contact : Feng Liang Life Technologies, a
                     division of Invitrogen 9800 Medical Center Drive Rockville
                     , Maryland 20850, USA Fax : (1) 301 610 8371 Email :
                     fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      215 a    201 c    211 g    221 t      1 others
ORIGIN
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Qy     78 CGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTG 137
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 05:25:37 ; Search time 119.279 Seconds
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Searched: 442118 seqs, 280819700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 884236

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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|---|---|---|---|---|---|---|---|
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| | 2 | 1968 | 93.6 | 2263 | 10 | US-09-765-231A-6 | Sequence 6, Appli |
| c | 3 | 279 | 13.3 | 586 | 10 | US-09-964-824A-446 | Sequence 446, App |
| | 4 | 241 | 11.5 | 368 | 10 | US-09-867-701-9693 | Sequence 9693, Ap |
| c | 5 | 240 | 11.4 | 479 | 10 | US-09-815-343-1286 | Sequence 1286, Ap |
| c | 6 | 221 | 10.5 | 221 | 9 | US-10-046-935-1922 | Sequence 1922, Ap |
| c | 7 | 221 | 10.5 | 221 | 9 | US-09-878-178-1922 | Sequence 1922, Ap |
| | 8 | 196 | 9.3 | 548 | 10 | US-09-925-299-368 | Sequence 368, App |
| | 9 | 115 | 5.5 | 747 | 9 | US-09-925-664-26 | Sequence 26, Appl |
| | 10 | 114 | 5.4 | 134 | 9 | US-09-925-664-22 | Sequence 22, Appl |
| c | 11 | 114 | 5.4 | 134 | 9 | US-09-925-664-23 | Sequence 23, Appl |
| | 12 | 114 | 5.4 | 300 | 9 | US-09-925-664-24 | Sequence 24, Appl |
| | 13 | 114 | 5.4 | 786 | 9 | US-09-925-664-29 | Sequence 29, Appl |
| | 14 | 71 | 3.4 | 418 | 10 | US-09-729-835-36 | Sequence 36, Appl |
| | 15 | 22 | 1.0 | 22 | 10 | US-09-799-952-1 | Sequence 1, Appli |
| c | 16 | 22 | 1.0 | 22 | 10 | US-09-799-952-2 | Sequence 2, Appli |
| | 17 | 21 | 1.0 | 198 | 10 | US-09-864-761-18005 | Sequence 18005, A |
| | 18 | 21 | 1.0 | 448 | 10 | US-09-864-761-1244 | Sequence 1244, Ap |
| | 19 | 20 | 1.0 | 1561 | 10 | US-09-765-272-121 | Sequence 121, App |
| | 20 | 20 | 1.0 | 2811 | 9 | US-09-759-130B-303 | Sequence 303, App |
| | 21 | 20 | 1.0 | 3121 | 10 | US-09-765-272-117 | Sequence 117, App |
| | 22 | 20 | 1.0 | 5119 | 9 | US-09-887-540A-1 | Sequence 1, Appli |
| c | 23 | 20 | 1.0 | 7326 | 12 | US-10-109-886-7 | Sequence 7, Appli |
| | 24 | 20 | 1.0 | 8095 | 9 | US-09-989-920-73 | Sequence 73, Appl |
| | 25 | 20 | 1.0 | 53542 | 10 | US-09-801-574-61 | Sequence 61, Appl |
| | 26 | 19 | 0.9 | 34 | 10 | US-09-263-959-803 | Sequence 803, App |
| c | 27 | 19 | 0.9 | 252 | 9 | US-09-796-692-8663 | Sequence 8663, Ap |
| c | 28 | 19 | 0.9 | 260 | 9 | US-09-796-692-8646 | Sequence 8646, Ap |
| c | 29 | 19 | 0.9 | 561 | 9 | US-09-796-692-4222 | Sequence 4222, Ap |
| | 30 | 19 | 0.9 | 1839 | 10 | US-09-938-970-3 | Sequence 3, Appli |
| c | 31 | 19 | 0.9 | 2000 | 9 | US-09-938-842A-5336 | Sequence 5336, Ap |
| | 32 | 19 | 0.9 | 2259 | 10 | US-09-964-824A-577 | Sequence 577, App |
| | 33 | 19 | 0.9 | 2259 | 10 | US-09-880-107-2107 | Sequence 2107, Ap |
| | 34 | 19 | 0.9 | 2259 | 10 | US-09-967-768A-137 | Sequence 137, App |
| c | 35 | 19 | 0.9 | 2267 | 9 | US-09-961-077-25 | Sequence 25, Appl |
| | 36 | 19 | 0.9 | 2389 | 10 | US-09-800-729-51 | Sequence 51, Appl |
| | 37 | 19 | 0.9 | 2464 | 10 | US-09-800-729-214 | Sequence 214, App |
| c | 38 | 19 | 0.9 | 2848 | 10 | US-09-939-980-197 | Sequence 197, App |
| | 39 | 19 | 0.9 | 2919 | 10 | US-09-765-344-1 | Sequence 1, Appli |
| | 40 | 19 | 0.9 | 2932 | 10 | US-09-938-970-1 | Sequence 1, Appli |
| | 41 | 19 | 0.9 | 2955 | 10 | US-09-765-344-2 | Sequence 2, Appli |
| | 42 | 19 | 0.9 | 3034 | 9 | US-10-051-186-1 | Sequence 1, Appli |
| c | 43 | 19 | 0.9 | 9797 | 10 | US-09-070-927A-550 | Sequence 550, App |
| | 44 | 19 | 0.9 | 26928 | 10 | US-09-880-107-2278 | Sequence 2278, Ap |
| | 45 | 19 | 0.9 | 31766 | 10 | US-09-765-344-5 | Sequence 5, Appli |
| | 46 | 19 | 0.9 | 43360 | 9 | US-10-114-170-206 | Sequence 206, App |
| | 47 | 19 | 0.9 | 45325 | 9 | US-10-114-170-261 | Sequence 261, App |
| | 48 | 19 | 0.9 | 659158 | 9 | US-09-771-208-20 | Sequence 20, Appl |
| | 49 | 19 | 0.9 | 684973 | 10 | US-09-263-959-1 | Sequence 1, Appli |
| c | 50 | 18 | 0.9 | 28 | 9 | US-09-925-664-25 | Sequence 25, Appl |
| | 51 | 18 | 0.9 | 101 | 10 | US-09-878-574-11549 | Sequence 11549, A |
| | 52 | 18 | 0.9 | 202 | 10 | US-09-864-761-24619 | Sequence 24619, A |
| c | 53 | 18 | 0.9 | 225 | 10 | US-09-815-242-9260 | Sequence 9260, Ap |
| | 54 | 18 | 0.9 | 277 | 10 | US-09-878-574-14647 | Sequence 14647, A |
| c | 55 | 18 | 0.9 | 411 | 10 | US-09-960-352-12687 | Sequence 12687, A |
| c | 56 | 18 | 0.9 | 594 | 10 | US-09-924-035A-394 | Sequence 394, App |
| | 57 | 18 | 0.9 | 600 | 10 | US-09-864-761-7915 | Sequence 7915, Ap |
| | 58 | 18 | 0.9 | 723 | 10 | US-09-770-149-136 | Sequence 136, App |
| c | 59 | 18 | 0.9 | 1296 | 10 | US-09-815-242-9082 | Sequence 9082, Ap |
| c | 60 | 18 | 0.9 | 1296 | 10 | US-09-815-242-9541 | Sequence 9541, Ap |
| c | 61 | 18 | 0.9 | 1721 | 12 | US-10-044-090-263 | Sequence 263, App |
| c | 62 | 18 | 0.9 | 1812 | 12 | US-10-044-090-264 | Sequence 264, App |
| | 63 | 18 | 0.9 | 1968 | 9 | US-10-066-521-12 | Sequence 12, Appl |
| c | 64 | 18 | 0.9 | 2000 | 9 | US-09-938-842A-4325 | Sequence 4325, Ap |
| | 65 | 18 | 0.9 | 2421 | 10 | US-09-815-242-6960 | Sequence 6960, Ap |
| c | 66 | 18 | 0.9 | 4400 | 10 | US-09-853-386-47 | Sequence 47, Appl |
| c | 67 | 18 | 0.9 | 4400 | 12 | US-10-005-169-3 | Sequence 3, Appli |
| c | 68 | 18 | 0.9 | 5222 | 10 | US-09-416-384A-1 | Sequence 1, Appli |
| c | 69 | 18 | 0.9 | 5566 | 10 | US-09-416-384A-4 | Sequence 4, Appli |
| | 70 | 18 | 0.9 | 5924 | 9 | US-10-041-856-2 | Sequence 2, Appli |
| | 71 | 18 | 0.9 | 6147 | 9 | US-09-953-572A-1 | Sequence 1, Appli |
| c | 72 | 18 | 0.9 | 56737 | 10 | US-09-782-378A-17 | Sequence 17, Appl |
| | 73 | 18 | 0.9 | 66479 | 9 | US-10-041-856-1 | Sequence 1, Appli |
| | 74 | 18 | 0.9 | 75899 | 10 | US-09-854-883-243 | Sequence 243, App |
| | 75 | 18 | 0.9 | 513509 | 9 | US-09-754-853A-4 | Sequence 4, Appli |
| | 76 | 17 | 0.8 | 22 | 10 | US-09-888-615-120 | Sequence 120, App |
| c | 77 | 17 | 0.8 | 28 | 9 | US-09-925-664-28 | Sequence 28, Appl |
| c | 78 | 17 | 0.8 | 110 | 10 | US-09-878-574-2595 | Sequence 2595, Ap |
| c | 79 | 17 | 0.8 | 112 | 10 | US-09-878-574-13385 | Sequence 13385, A |
| c | 80 | 17 | 0.8 | 189 | 10 | US-09-864-761-21705 | Sequence 21705, A |
| | 81 | 17 | 0.8 | 208 | 10 | US-09-764-847-1017 | Sequence 1017, Ap |
| c | 82 | 17 | 0.8 | 240 | 10 | US-09-294-093B-5714 | Sequence 5714, Ap |
| c | 83 | 17 | 0.8 | 251 | 9 | US-10-040-739-33 | Sequence 33, Appl |
| c | 84 | 17 | 0.8 | 286 | 10 | US-09-563-817-848 | Sequence 848, App |
| c | 85 | 17 | 0.8 | 355 | 10 | US-09-969-347-112 | Sequence 112, App |
| | 86 | 17 | 0.8 | 377 | 10 | US-09-867-701-6350 | Sequence 6350, Ap |
| | 87 | 17 | 0.8 | 378 | 9 | US-09-736-457-770 | Sequence 770, App |
| | 88 | 17 | 0.8 | 378 | 9 | US-09-902-941-770 | Sequence 770, App |
| | 89 | 17 | 0.8 | 378 | 9 | US-09-849-626-770 | Sequence 770, App |
| | 90 | 17 | 0.8 | 396 | 9 | US-09-970-966-29 | Sequence 29, Appl |
| | 91 | 17 | 0.8 | 396 | 10 | US-09-825-294-29 | Sequence 29, Appl |
| | 92 | 17 | 0.8 | 401 | 10 | US-09-735-705-266 | Sequence 266, App |

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|---|---|---|---|---|---|---|
| | 93 | 17 | 0.8 | 401 | 10 | US-09-850-716A-266 | Sequence 266, App |
| | 94 | 17 | 0.8 | 401 | 10 | US-09-897-778-266 | Sequence 266, App |
| c | 95 | 17 | 0.8 | 406 | 10 | US-09-960-352-10265 | Sequence 10265, A |
| | 96 | 17 | 0.8 | 407 | 10 | US-09-864-761-11446 | Sequence 11446, A |
| c | 97 | 17 | 0.8 | 416 | 10 | US-09-867-701-5340 | Sequence 5340, Ap |
| | 98 | 17 | 0.8 | 421 | 10 | US-09-833-381-1167 | Sequence 1167, Ap |
| | 99 | 17 | 0.8 | 429 | 10 | US-09-960-352-1464 | Sequence 1464, Ap |
| c | 100 | 17 | 0.8 | 444 | 10 | US-09-864-761-10036 | Sequence 10036, A |
| c | 101 | 17 | 0.8 | 458 | 10 | US-09-960-352-14274 | Sequence 14274, A |
| | 102 | 17 | 0.8 | 460 | 10 | US-09-960-352-10251 | Sequence 10251, A |
| | 103 | 17 | 0.8 | 473 | 9 | US-10-046-935-837 | Sequence 837, App |
| | 104 | 17 | 0.8 | 473 | 9 | US-09-878-178-837 | Sequence 837, App |
| c | 105 | 17 | 0.8 | 483 | 9 | US-10-046-935-1306 | Sequence 1306, Ap |
| c | 106 | 17 | 0.8 | 483 | 9 | US-09-878-178-1306 | Sequence 1306, Ap |
| c | 107 | 17 | 0.8 | 489 | 10 | US-09-864-761-1722 | Sequence 1722, Ap |
| c | 108 | 17 | 0.8 | 489 | 10 | US-09-864-761-4976 | Sequence 4976, Ap |
| | 109 | 17 | 0.8 | 496 | 10 | US-09-764-869-35 | Sequence 35, Appl |
| c | 110 | 17 | 0.8 | 546 | 10 | US-09-864-761-8050 | Sequence 8050, Ap |
| | 111 | 17 | 0.8 | 551 | 10 | US-09-852-137-1 | Sequence 1, Appli |
| | 112 | 17 | 0.8 | 553 | 10 | US-09-764-853-317 | Sequence 317, App |
| | 113 | 17 | 0.8 | 554 | 10 | US-09-917-800A-655 | Sequence 655, App |
| c | 114 | 17 | 0.8 | 560 | 9 | US-09-764-904-17 | Sequence 17, Appl |
| c | 115 | 17 | 0.8 | 560 | 10 | US-09-764-860-269 | Sequence 269, App |
| | 116 | 17 | 0.8 | 572 | 10 | US-09-864-761-11928 | Sequence 11928, A |
| c | 117 | 17 | 0.8 | 591 | 9 | US-09-796-692-8514 | Sequence 8514, Ap |
| | 118 | 17 | 0.8 | 627 | 10 | US-09-853-666-1 | Sequence 1, Appli |
| | 119 | 17 | 0.8 | 631 | 10 | US-09-770-149-681 | Sequence 681, App |
| | 120 | 17 | 0.8 | 651 | 10 | US-09-811-284-57 | Sequence 57, Appl |
| | 121 | 17 | 0.8 | 788 | 10 | US-09-910-943-393 | Sequence 393, App |
| c | 122 | 17 | 0.8 | 863 | 10 | US-09-834-975-901 | Sequence 901, App |
| c | 123 | 17 | 0.8 | 916 | 10 | US-09-790-099-6 | Sequence 6, Appli |
| | 124 | 17 | 0.8 | 939 | 10 | US-09-731-872-97 | Sequence 97, Appl |
| c | 125 | 17 | 0.8 | 966 | 9 | US-10-114-893-3 | Sequence 3, Appli |
| | 126 | 17 | 0.8 | 1008 | 10 | US-09-974-300-52 | Sequence 52, Appl |
| c | 127 | 17 | 0.8 | 1065 | 10 | US-09-801-368-413 | Sequence 413, App |
| c | 128 | 17 | 0.8 | 1093 | 10 | US-09-799-777-126 | Sequence 126, App |
| c | 129 | 17 | 0.8 | 1120 | 10 | US-09-925-300-595 | Sequence 595, App |
| | 130 | 17 | 0.8 | 1124 | 10 | US-09-770-445-88 | Sequence 88, Appl |
| | 131 | 17 | 0.8 | 1200 | 10 | US-09-887-576-717 | Sequence 717, App |
| | 132 | 17 | 0.8 | 1210 | 10 | US-09-899-980A-12 | Sequence 12, Appl |
| c | 133 | 17 | 0.8 | 1282 | 10 | US-09-764-864-288 | Sequence 288, App |
| | 134 | 17 | 0.8 | 1344 | 12 | US-10-062-254-287 | Sequence 287, App |
| | 135 | 17 | 0.8 | 1347 | 10 | US-09-923-246-105 | Sequence 105, App |
| c | 136 | 17 | 0.8 | 1354 | 9 | US-10-114-893-5 | Sequence 5, Appli |
| | 137 | 17 | 0.8 | 1357 | 10 | US-09-899-980A-5 | Sequence 5, Appli |
| c | 138 | 17 | 0.8 | 1380 | 9 | US-09-738-626-723 | Sequence 723, App |
| | 139 | 17 | 0.8 | 1383 | 9 | US-09-970-989-6 | Sequence 6, Appli |
| | 140 | 17 | 0.8 | 1383 | 10 | US-09-967-768A-189 | Sequence 189, App |
| | 141 | 17 | 0.8 | 1455 | 10 | US-09-917-265-104 | Sequence 104, App |
| c | 142 | 17 | 0.8 | 1455 | 10 | US-09-917-265-106 | Sequence 106, App |
| | 143 | 17 | 0.8 | 1522 | 9 | US-09-954-531-612 | Sequence 612, App |
| | 144 | 17 | 0.8 | 1522 | 10 | US-09-962-436-20 | Sequence 20, Appl |
| | 145 | 17 | 0.8 | 1590 | 10 | US-09-888-615-3 | Sequence 3, Appli |
| | 146 | 17 | 0.8 | 1616 | 9 | US-09-938-842A-3086 | Sequence 3086, Ap |
| | 147 | 17 | 0.8 | 1659 | 9 | US-09-938-842A-4435 | Sequence 4435, Ap |
| | 148 | 17 | 0.8 | 1680 | 10 | US-09-899-980A-10 | Sequence 10, Appl |
| | 149 | 17 | 0.8 | 1723 | 9 | US-09-938-842A-3127 | Sequence 3127, Ap |
| c | 150 | 17 | 0.8 | 1791 | 10 | US-09-880-107-3385 | Sequence 3385, Ap |
| | 151 | 17 | 0.8 | 1902 | 10 | US-09-917-800A-480 | Sequence 480, App |
| | 152 | 17 | 0.8 | 1918 | 10 | US-09-880-192-7 | Sequence 7, Appli |
| | 153 | 17 | 0.8 | 1918 | 10 | US-09-880-192-39 | Sequence 39, Appl |
| c | 154 | 17 | 0.8 | 1931 | 10 | US-09-925-301-454 | Sequence 454, App |
| | 155 | 17 | 0.8 | 1960 | 12 | US-10-044-090-234 | Sequence 234, App |
| | 156 | 17 | 0.8 | 2000 | 9 | US-09-938-842A-3113 | Sequence 3113, Ap |
| | 157 | 17 | 0.8 | 2000 | 9 | US-09-938-842A-4502 | Sequence 4502, Ap |
| | 158 | 17 | 0.8 | 2000 | 9 | US-09-938-842A-4794 | Sequence 4794, Ap |
| c | 159 | 17 | 0.8 | 2000 | 9 | US-09-938-842A-5000 | Sequence 5000, Ap |
| | 160 | 17 | 0.8 | 2058 | 10 | US-09-899-980A-4 | Sequence 4, Appli |
| c | 161 | 17 | 0.8 | 2167 | 10 | US-09-452-599-16 | Sequence 16, Appl |
| | 162 | 17 | 0.8 | 2405 | 10 | US-09-800-729-17 | Sequence 17, Appl |
| c | 163 | 17 | 0.8 | 2411 | 9 | US-09-764-904-89 | Sequence 89, Appl |
| c | 164 | 17 | 0.8 | 2411 | 10 | US-09-764-860-1133 | Sequence 1133, Ap |
| c | 165 | 17 | 0.8 | 2779 | 10 | US-09-070-927A-235 | Sequence 235, App |
| | 166 | 17 | 0.8 | 3010 | 9 | US-09-992-598-313 | Sequence 313, App |
| | 167 | 17 | 0.8 | 3010 | 9 | US-09-989-293A-313 | Sequence 313, App |
| | 168 | 17 | 0.8 | 3010 | 9 | US-09-989-735-313 | Sequence 313, App |
| | 169 | 17 | 0.8 | 3010 | 9 | US-09-990-444-313 | Sequence 313, App |
| | 170 | 17 | 0.8 | 3010 | 9 | US-09-989-730-313 | Sequence 313, App |
| | 171 | 17 | 0.8 | 3010 | 9 | US-09-990-436-313 | Sequence 313, App |
| | 172 | 17 | 0.8 | 3010 | 9 | US-09-991-181-313 | Sequence 313, App |
| | 173 | 17 | 0.8 | 3010 | 9 | US-09-993-687-313 | Sequence 313, App |
| | 174 | 17 | 0.8 | 3010 | 9 | US-09-989-734-313 | Sequence 313, App |
| | 175 | 17 | 0.8 | 3010 | 9 | US-09-997-653-313 | Sequence 313, App |
| | 176 | 17 | 0.8 | 3010 | 9 | US-09-993-667-313 | Sequence 313, App |
| | 177 | 17 | 0.8 | 3010 | 9 | US-09-990-438-313 | Sequence 313, App |
| | 178 | 17 | 0.8 | 3010 | 9 | US-09-990-562-313 | Sequence 313, App |
| | 179 | 17 | 0.8 | 3010 | 9 | US-09-997-428-313 | Sequence 313, App |
| | 180 | 17 | 0.8 | 3010 | 9 | US-09-997-666-313 | Sequence 313, App |
| | 181 | 17 | 0.8 | 3010 | 9 | US-09-990-711-313 | Sequence 313, App |
| | 182 | 17 | 0.8 | 3010 | 10 | US-09-989-722-313 | Sequence 313, App |
| | 183 | 17 | 0.8 | 3010 | 10 | US-09-989-723-313 | Sequence 313, App |
| | 184 | 17 | 0.8 | 3010 | 10 | US-09-989-279-313 | Sequence 313, App |
| | 185 | 17 | 0.8 | 3010 | 10 | US-09-989-727-313 | Sequence 313, App |
| | 186 | 17 | 0.8 | 3010 | 10 | US-09-989-731-313 | Sequence 313, App |
| | 187 | 17 | 0.8 | 3010 | 10 | US-09-989-732-313 | Sequence 313, App |
| | 188 | 17 | 0.8 | 3010 | 10 | US-09-991-073-313 | Sequence 313, App |
| | 189 | 17 | 0.8 | 3010 | 10 | US-09-990-442-313 | Sequence 313, App |
| | 190 | 17 | 0.8 | 3010 | 10 | US-09-991-163-313 | Sequence 313, App |
| | 191 | 17 | 0.8 | 3010 | 10 | US-09-993-604-313 | Sequence 313, App |
| | 192 | 17 | 0.8 | 3010 | 10 | US-09-990-456-313 | Sequence 313, App |
| | 193 | 17 | 0.8 | 3010 | 10 | US-09-989-721-313 | Sequence 313, App |
| | 194 | 17 | 0.8 | 3474 | 10 | US-09-925-302-143 | Sequence 143, App |
| | 195 | 17 | 0.8 | 3502 | 9 | US-10-098-841-48 | Sequence 48, Appl |
| | 196 | 17 | 0.8 | 3772 | 9 | US-09-992-598-61 | Sequence 61, Appl |
| | 197 | 17 | 0.8 | 3772 | 9 | US-09-989-293A-61 | Sequence 61, Appl |
| | 198 | 17 | 0.8 | 3772 | 9 | US-09-989-735-61 | Sequence 61, Appl |
| | 199 | 17 | 0.8 | 3772 | 9 | US-09-990-444-61 | Sequence 61, Appl |
| | 200 | 17 | 0.8 | 3772 | 9 | US-09-989-730-61 | Sequence 61, Appl |
| | 201 | 17 | 0.8 | 3772 | 9 | US-09-990-436-61 | Sequence 61, Appl |
| | 202 | 17 | 0.8 | 3772 | 9 | US-09-991-181-61 | Sequence 61, Appl |
| | 203 | 17 | 0.8 | 3772 | 9 | US-09-993-687-61 | Sequence 61, Appl |
| | 204 | 17 | 0.8 | 3772 | 9 | US-09-989-734-61 | Sequence 61, Appl |
| | 205 | 17 | 0.8 | 3772 | 9 | US-10-028-072-391 | Sequence 391, App |
| | 206 | 17 | 0.8 | 3772 | 9 | US-09-997-653-61 | Sequence 61, Appl |
| | 207 | 17 | 0.8 | 3772 | 9 | US-09-993-667-61 | Sequence 61, Appl |
| | 208 | 17 | 0.8 | 3772 | 9 | US-10-121-049-391 | Sequence 391, App |
| | 209 | 17 | 0.8 | 3772 | 9 | US-10-123-904-391 | Sequence 391, App |
| | 210 | 17 | 0.8 | 3772 | 9 | US-10-140-470-391 | Sequence 391, App |
| | 211 | 17 | 0.8 | 3772 | 9 | US-09-990-438-61 | Sequence 61, Appl |
| | 212 | 17 | 0.8 | 3772 | 9 | US-09-990-562-61 | Sequence 61, Appl |
| | 213 | 17 | 0.8 | 3772 | 9 | US-09-997-428-61 | Sequence 61, Appl |
| | 214 | 17 | 0.8 | 3772 | 9 | US-09-997-666-61 | Sequence 61, Appl |
| | 215 | 17 | 0.8 | 3772 | 9 | US-10-175-746-391 | Sequence 391, App |
| | 216 | 17 | 0.8 | 3772 | 9 | US-10-176-918-391 | Sequence 391, App |
| | 217 | 17 | 0.8 | 3772 | 9 | US-10-176-921-391 | Sequence 391, App |
| | 218 | 17 | 0.8 | 3772 | 9 | US-09-990-711-61 | Sequence 61, Appl |
| | 219 | 17 | 0.8 | 3772 | 9 | US-10-137-865-391 | Sequence 391, App |
| | 220 | 17 | 0.8 | 3772 | 9 | US-10-140-474-391 | Sequence 391, App |
| | 221 | 17 | 0.8 | 3772 | 10 | US-09-989-722-61 | Sequence 61, Appl |
| | 222 | 17 | 0.8 | 3772 | 10 | US-09-989-723-61 | Sequence 61, Appl |
| | 223 | 17 | 0.8 | 3772 | 10 | US-09-989-279-61 | Sequence 61, Appl |
| | 224 | 17 | 0.8 | 3772 | 10 | US-09-989-727-61 | Sequence 61, Appl |
| | 225 | 17 | 0.8 | 3772 | 10 | US-09-989-731-61 | Sequence 61, Appl |
| | 226 | 17 | 0.8 | 3772 | 10 | US-09-989-732-61 | Sequence 61, Appl |
| | 227 | 17 | 0.8 | 3772 | 10 | US-09-991-073-61 | Sequence 61, Appl |
| | 228 | 17 | 0.8 | 3772 | 10 | US-09-990-442-61 | Sequence 61, Appl |
| | 229 | 17 | 0.8 | 3772 | 10 | US-09-991-163-61 | Sequence 61, Appl |
| | 230 | 17 | 0.8 | 3772 | 10 | US-09-993-604-61 | Sequence 61, Appl |
| | 231 | 17 | 0.8 | 3772 | 10 | US-09-990-456-61 | Sequence 61, Appl |
| | 232 | 17 | 0.8 | 3772 | 10 | US-09-989-721-61 | Sequence 61, Appl |
| c | 233 | 17 | 0.8 | 3805 | 10 | US-09-834-975-993 | Sequence 993, App |
| | 234 | 17 | 0.8 | 3810 | 10 | US-09-925-301-164 | Sequence 164, App |
| | 235 | 17 | 0.8 | 4355 | 9 | US-09-843-250-7 | Sequence 7, Appli |
| | 236 | 17 | 0.8 | 4369 | 10 | US-09-764-877-2824 | Sequence 2824, Ap |
| | 237 | 17 | 0.8 | 4376 | 10 | US-09-875-724-1 | Sequence 1, Appli |
| c | 238 | 17 | 0.8 | 4526 | 9 | US-10-108-605-112 | Sequence 112, App |

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|---|---|---|---|---|---|---|
| c 239 | 17 | 0.8 | 5387 | 9 | US-10-001-873-22 | Sequence 22, Appl |
| c 240 | 17 | 0.8 | 5510 | 10 | US-09-880-107-1758 | Sequence 1758, Ap |
| c 241 | 17 | 0.8 | 6659 | 10 | US-09-321-987B-1 | Sequence 1, Appli |
| 242 | 17 | 0.8 | 7071 | 10 | US-09-954-456-1881 | Sequence 1881, Ap |
| c 243 | 17 | 0.8 | 7869 | 10 | US-09-954-456-1921 | Sequence 1921, Ap |
| 244 | 17 | 0.8 | 7923 | 10 | US-09-864-864-297 | Sequence 297, App |
| 245 | 17 | 0.8 | 9279 | 10 | US-09-801-368-171 | Sequence 171, App |
| c 246 | 17 | 0.8 | 10519 | 10 | US-09-764-847-1628 | Sequence 1628, Ap |
| c 247 | 17 | 0.8 | 11464 | 12 | US-10-100-057-17 | Sequence 17, Appl |
| c 248 | 17 | 0.8 | 11597 | 10 | US-09-070-927A-222 | Sequence 222, App |
| c 249 | 17 | 0.8 | 13337 | 10 | US-09-764-846-312 | Sequence 312, App |
| c 250 | 17 | 0.8 | 13337 | 10 | US-09-764-847-1629 | Sequence 1629, Ap |
| 251 | 17 | 0.8 | 13932 | 10 | US-09-070-927A-363 | Sequence 363, App |
| 252 | 17 | 0.8 | 15643 | 10 | US-09-764-870-638 | Sequence 638, App |
| c 253 | 17 | 0.8 | 32191 | 10 | US-09-764-864-1678 | Sequence 1678, Ap |
| 254 | 17 | 0.8 | 32191 | 10 | US-09-764-877-3374 | Sequence 3374, Ap |
| 255 | 17 | 0.8 | 32193 | 10 | US-09-764-877-2147 | Sequence 2147, Ap |
| c 256 | 17 | 0.8 | 110096 | 10 | US-09-880-107-1542 | Sequence 1542, Ap |
| 257 | 16 | 0.8 | 71 | 9 | US-10-015-219-847 | Sequence 847, App |
| 258 | 16 | 0.8 | 71 | 10 | US-09-777-564-847 | Sequence 847, App |
| 259 | 16 | 0.8 | 99 | 9 | US-09-736-457-1291 | Sequence 1291, Ap |
| 260 | 16 | 0.8 | 99 | 9 | US-09-902-941-1291 | Sequence 1291, Ap |
| 261 | 16 | 0.8 | 99 | 9 | US-09-849-626-1291 | Sequence 1291, Ap |
| 262 | 16 | 0.8 | 116 | 10 | US-09-969-373-1164 | Sequence 1164, Ap |
| c 263 | 16 | 0.8 | 122 | 10 | US-09-864-761-29547 | Sequence 29547, A |
| 264 | 16 | 0.8 | 184 | 10 | US-09-765-231A-48 | Sequence 48, Appl |
| 265 | 16 | 0.8 | 188 | 10 | US-09-783-590-5330 | Sequence 5330, Ap |
| c 266 | 16 | 0.8 | 190 | 10 | US-09-867-701-6909 | Sequence 6909, Ap |
| 267 | 16 | 0.8 | 193 | 10 | US-09-960-352-8906 | Sequence 8906, Ap |
| 268 | 16 | 0.8 | 195 | 10 | US-09-960-352-11978 | Sequence 11978, A |
| 269 | 16 | 0.8 | 199 | 9 | US-09-933-797-733 | Sequence 733, App |
| 270 | 16 | 0.8 | 199 | 10 | US-09-923-876-2150 | Sequence 2150, Ap |
| 271 | 16 | 0.8 | 231 | 9 | US-09-796-692-3380 | Sequence 3380, Ap |
| c 272 | 16 | 0.8 | 241 | 10 | US-09-878-574-6915 | Sequence 6915, Ap |
| 273 | 16 | 0.8 | 249 | 10 | US-09-778-320-228 | Sequence 228, App |
| 274 | 16 | 0.8 | 249 | 10 | US-09-910-689-228 | Sequence 228, App |
| 275 | 16 | 0.8 | 249 | 12 | US-10-010-742-228 | Sequence 228, App |
| c 276 | 16 | 0.8 | 250 | 10 | US-09-881-752A-213 | Sequence 213, App |
| c 277 | 16 | 0.8 | 255 | 10 | US-09-728-446-532 | Sequence 532, App |
| c 278 | 16 | 0.8 | 259 | 10 | US-09-878-574-11411 | Sequence 11411, A |
| c 279 | 16 | 0.8 | 265 | 10 | US-09-878-574-6639 | Sequence 6639, Ap |
| c 280 | 16 | 0.8 | 267 | 9 | US-10-015-219-1405 | Sequence 1405, Ap |
| 281 | 16 | 0.8 | 267 | 9 | US-10-015-219-1586 | Sequence 1586, Ap |
| c 282 | 16 | 0.8 | 267 | 10 | US-09-777-564-1405 | Sequence 1405, Ap |
| 283 | 16 | 0.8 | 267 | 10 | US-09-777-564-1586 | Sequence 1586, Ap |
| c 284 | 16 | 0.8 | 272 | 10 | US-09-878-574-11034 | Sequence 11034, A |
| c 285 | 16 | 0.8 | 275 | 10 | US-09-878-574-9787 | Sequence 9787, Ap |
| 286 | 16 | 0.8 | 276 | 10 | US-09-867-701-9006 | Sequence 9006, Ap |
| c 287 | 16 | 0.8 | 291 | 10 | US-09-294-093B-1297 | Sequence 1297, Ap |
| 288 | 16 | 0.8 | 297 | 9 | US-09-796-692-3405 | Sequence 3405, Ap |
| c 289 | 16 | 0.8 | 299 | 9 | US-10-015-219-1000 | Sequence 1000, Ap |
| c 290 | 16 | 0.8 | 299 | 10 | US-09-777-564-1000 | Sequence 1000, Ap |
| 291 | 16 | 0.8 | 302 | 9 | US-09-728-444-99 | Sequence 99, Appl |
| c 292 | 16 | 0.8 | 304 | 9 | US-10-040-739-1139 | Sequence 1139, Ap |
| 293 | 16 | 0.8 | 309 | 9 | US-09-938-842A-2284 | Sequence 2284, Ap |
| c 294 | 16 | 0.8 | 341 | 10 | US-09-983-965-4676 | Sequence 4676, Ap |
| 295 | 16 | 0.8 | 345 | 10 | US-09-878-574-3086 | Sequence 3086, Ap |
| 296 | 16 | 0.8 | 347 | 10 | US-09-983-646A-3 | Sequence 3, Appli |
| 297 | 16 | 0.8 | 350 | 10 | US-09-960-352-2939 | Sequence 2939, Ap |
| 298 | 16 | 0.8 | 351 | 10 | US-09-815-242-4231 | Sequence 4231, Ap |
| 299 | 16 | 0.8 | 351 | 10 | US-09-960-352-5800 | Sequence 5800, Ap |
| 300 | 16 | 0.8 | 351 | 10 | US-09-974-300-7989 | Sequence 7989, Ap |
| c 301 | 16 | 0.8 | 352 | 10 | US-09-867-701-147 | Sequence 147, App |
| c 302 | 16 | 0.8 | 354 | 9 | US-09-796-692-9065 | Sequence 9065, Ap |
| 303 | 16 | 0.8 | 357 | 9 | US-09-938-842A-1736 | Sequence 1736, Ap |
| c 304 | 16 | 0.8 | 360 | 10 | US-09-864-761-27334 | Sequence 27334, A |
| 305 | 16 | 0.8 | 365 | 10 | US-09-960-352-8638 | Sequence 8638, Ap |
| c 306 | 16 | 0.8 | 367 | 10 | US-09-880-107-1256 | Sequence 1256, Ap |
| c 307 | 16 | 0.8 | 370 | 10 | US-09-867-550-1011 | Sequence 1011, Ap |
| c 308 | 16 | 0.8 | 380 | 10 | US-09-878-574-2372 | Sequence 2372, Ap |
| 309 | 16 | 0.8 | 387 | 10 | US-09-983-965-3850 | Sequence 3850, Ap |
| 310 | 16 | 0.8 | 388 | 10 | US-09-878-574-3118 | Sequence 3118, Ap |
| 311 | 16 | 0.8 | 388 | 10 | US-09-878-574-3119 | Sequence 3119, Ap |
| 312 | 16 | 0.8 | 395 | 10 | US-09-969-708-531 | Sequence 531, App |
| 313 | 16 | 0.8 | 396 | 9 | US-09-970-966-13 | Sequence 13, Appl |
| 314 | 16 | 0.8 | 396 | 10 | US-09-825-294-13 | Sequence 13, Appl |
| c 315 | 16 | 0.8 | 398 | 10 | US-09-960-352-5047 | Sequence 5047, Ap |
| 316 | 16 | 0.8 | 399 | 10 | US-09-867-701-4588 | Sequence 4588, Ap |
| c 317 | 16 | 0.8 | 400 | 10 | US-09-878-574-2200 | Sequence 2200, Ap |
| 318 | 16 | 0.8 | 401 | 9 | US-09-946-807-381 | Sequence 381, App |
| 319 | 16 | 0.8 | 401 | 9 | US-09-946-807-734 | Sequence 734, App |
| 320 | 16 | 0.8 | 401 | 10 | US-09-795-668-381 | Sequence 381, App |
| 321 | 16 | 0.8 | 401 | 10 | US-09-795-668-734 | Sequence 734, App |
| 322 | 16 | 0.8 | 401 | 10 | US-09-795-686-381 | Sequence 381, App |
| 323 | 16 | 0.8 | 401 | 10 | US-09-795-686-734 | Sequence 734, App |
| 324 | 16 | 0.8 | 407 | 9 | US-09-933-797-759 | Sequence 759, App |
| 325 | 16 | 0.8 | 409 | 10 | US-09-878-574-2967 | Sequence 2967, Ap |
| 326 | 16 | 0.8 | 413 | 10 | US-09-864-761-981 | Sequence 981, App |
| c 327 | 16 | 0.8 | 417 | 10 | US-09-864-761-1969 | Sequence 1969, Ap |
| c 328 | 16 | 0.8 | 420 | 10 | US-09-983-965-32 | Sequence 32, Appl |
| c 329 | 16 | 0.8 | 425 | 10 | US-09-983-965-512 | Sequence 512, App |
| 330 | 16 | 0.8 | 431 | 10 | US-09-867-701-3628 | Sequence 3628, Ap |
| 331 | 16 | 0.8 | 431 | 10 | US-09-867-701-7253 | Sequence 7253, Ap |
| c 332 | 16 | 0.8 | 432 | 10 | US-09-867-701-1104 | Sequence 1104, Ap |
| c 333 | 16 | 0.8 | 435 | 10 | US-09-880-107-2652 | Sequence 2652, Ap |
| c 334 | 16 | 0.8 | 439 | 10 | US-09-864-761-20174 | Sequence 20174, A |
| c 335 | 16 | 0.8 | 441 | 10 | US-09-864-761-3403 | Sequence 3403, Ap |
| c 336 | 16 | 0.8 | 443 | 10 | US-09-967-768A-234 | Sequence 234, App |
| c 337 | 16 | 0.8 | 447 | 10 | US-09-960-352-8223 | Sequence 8223, Ap |
| c 338 | 16 | 0.8 | 448 | 10 | US-09-864-761-15549 | Sequence 15549, A |
| 339 | 16 | 0.8 | 451 | 10 | US-09-864-761-3501 | Sequence 3501, Ap |
| 340 | 16 | 0.8 | 451 | 10 | US-09-864-761-5869 | Sequence 5869, Ap |
| c 341 | 16 | 0.8 | 455 | 9 | US-10-015-219-62 | Sequence 62, Appl |
| c 342 | 16 | 0.8 | 455 | 10 | US-09-777-564-62 | Sequence 62, Appl |
| 343 | 16 | 0.8 | 456 | 10 | US-09-815-242-8409 | Sequence 8409, Ap |
| c 344 | 16 | 0.8 | 461 | 10 | US-09-962-436-51 | Sequence 51, Appl |
| 345 | 16 | 0.8 | 469 | 10 | US-09-864-761-704 | Sequence 704, App |
| 346 | 16 | 0.8 | 472 | 10 | US-09-864-761-13835 | Sequence 13835, A |
| 347 | 16 | 0.8 | 474 | 10 | US-09-864-761-1643 | Sequence 1643, Ap |
| 348 | 16 | 0.8 | 479 | 10 | US-09-920-300A-1754 | Sequence 1754, Ap |
| 349 | 16 | 0.8 | 479 | 12 | US-10-033-528-1754 | Sequence 1754, Ap |
| c 350 | 16 | 0.8 | 482 | 9 | US-10-021-162-62 | Sequence 62, Appl |
| c 351 | 16 | 0.8 | 488 | 10 | US-09-864-761-2643 | Sequence 2643, Ap |
| 352 | 16 | 0.8 | 496 | 9 | US-09-992-598-348 | Sequence 348, App |
| 353 | 16 | 0.8 | 496 | 9 | US-09-989-293A-348 | Sequence 348, App |
| 354 | 16 | 0.8 | 496 | 9 | US-09-989-735-348 | Sequence 348, App |
| 355 | 16 | 0.8 | 496 | 9 | US-09-990-444-348 | Sequence 348, App |
| 356 | 16 | 0.8 | 496 | 9 | US-09-989-730-348 | Sequence 348, App |
| 357 | 16 | 0.8 | 496 | 9 | US-09-990-436-348 | Sequence 348, App |
| 358 | 16 | 0.8 | 496 | 9 | US-09-991-181-348 | Sequence 348, App |
| 359 | 16 | 0.8 | 496 | 9 | US-09-993-687-348 | Sequence 348, App |
| 360 | 16 | 0.8 | 496 | 9 | US-09-989-734-348 | Sequence 348, App |
| 361 | 16 | 0.8 | 496 | 9 | US-09-997-653-348 | Sequence 348, App |
| 362 | 16 | 0.8 | 496 | 9 | US-09-993-667-348 | Sequence 348, App |
| 363 | 16 | 0.8 | 496 | 9 | US-09-990-438-348 | Sequence 348, App |
| 364 | 16 | 0.8 | 496 | 9 | US-09-990-562-348 | Sequence 348, App |
| 365 | 16 | 0.8 | 496 | 9 | US-09-997-428-348 | Sequence 348, App |
| 366 | 16 | 0.8 | 496 | 9 | US-09-997-666-348 | Sequence 348, App |
| 367 | 16 | 0.8 | 496 | 9 | US-09-990-711-348 | Sequence 348, App |
| c 368 | 16 | 0.8 | 496 | 10 | US-09-864-761-10689 | Sequence 10689, A |
| 369 | 16 | 0.8 | 496 | 10 | US-09-989-722-348 | Sequence 348, App |
| 370 | 16 | 0.8 | 496 | 10 | US-09-989-723-348 | Sequence 348, App |
| 371 | 16 | 0.8 | 496 | 10 | US-09-989-279-348 | Sequence 348, App |
| 372 | 16 | 0.8 | 496 | 10 | US-09-989-727-348 | Sequence 348, App |
| 373 | 16 | 0.8 | 496 | 10 | US-09-989-731-348 | Sequence 348, App |
| 374 | 16 | 0.8 | 496 | 10 | US-09-989-732-348 | Sequence 348, App |
| 375 | 16 | 0.8 | 496 | 10 | US-09-991-073-348 | Sequence 348, App |
| 376 | 16 | 0.8 | 496 | 10 | US-09-990-442-348 | Sequence 348, App |
| 377 | 16 | 0.8 | 496 | 10 | US-09-991-163-348 | Sequence 348, App |
| 378 | 16 | 0.8 | 496 | 10 | US-09-993-604-348 | Sequence 348, App |
| 379 | 16 | 0.8 | 496 | 10 | US-09-990-456-348 | Sequence 348, App |
| 380 | 16 | 0.8 | 496 | 10 | US-09-989-721-348 | Sequence 348, App |
| c 381 | 16 | 0.8 | 500 | 10 | US-09-917-800A-1273 | Sequence 1273, Ap |
| c 382 | 16 | 0.8 | 501 | 10 | US-09-920-300A-216 | Sequence 216, App |
| c 383 | 16 | 0.8 | 501 | 10 | US-09-920-300A-1657 | Sequence 1657, Ap |
| 384 | 16 | 0.8 | 501 | 10 | US-09-998-598-1102 | Sequence 1102, Ap |

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|---|---|---|---|---|---|---|
| c 385 | 16 | 0.8 | 501 | 12 | US-10-033-528-216 | Sequence 216, App |
| c 386 | 16 | 0.8 | 501 | 12 | US-10-033-528-1657 | Sequence 1657, Ap |
| 387 | 16 | 0.8 | 507 | 10 | US-09-880-107-553 | Sequence 553, App |
| 388 | 16 | 0.8 | 512 | 10 | US-09-998-598-798 | Sequence 798, App |
| 389 | 16 | 0.8 | 512 | 10 | US-09-998-598-1034 | Sequence 1034, Ap |
| 390 | 16 | 0.8 | 514 | 9 | US-09-854-133-282 | Sequence 282, App |
| 391 | 16 | 0.8 | 514 | 10 | US-09-738-973-282 | Sequence 282, App |
| c 392 | 16 | 0.8 | 521 | 10 | US-09-728-446-1398 | Sequence 1398, Ap |
| c 393 | 16 | 0.8 | 529 | 10 | US-09-878-574-4302 | Sequence 4302, Ap |
| c 394 | 16 | 0.8 | 545 | 10 | US-09-864-761-11836 | Sequence 11836, A |
| 395 | 16 | 0.8 | 545 | 10 | US-09-764-869-583 | Sequence 583, App |
| 396 | 16 | 0.8 | 547 | 9 | US-09-933-797-208 | Sequence 208, App |
| 397 | 16 | 0.8 | 548 | 10 | US-09-764-860-1059 | Sequence 1059, Ap |
| 398 | 16 | 0.8 | 548 | 10 | US-09-867-701-1427 | Sequence 1427, Ap |
| 399 | 16 | 0.8 | 551 | 10 | US-09-864-761-6982 | Sequence 6982, Ap |
| c 400 | 16 | 0.8 | 560 | 10 | US-09-867-701-1428 | Sequence 1428, Ap |
| c 401 | 16 | 0.8 | 574 | 9 | US-10-021-162-25 | Sequence 25, Appl |
| c 402 | 16 | 0.8 | 576 | 10 | US-09-764-870-125 | Sequence 125, App |
| 403 | 16 | 0.8 | 577 | 9 | US-10-002-344A-11 | Sequence 11, Appl |
| c 404 | 16 | 0.8 | 577 | 10 | US-09-864-761-12984 | Sequence 12984, A |
| c 405 | 16 | 0.8 | 588 | 10 | US-09-864-761-6697 | Sequence 6697, Ap |
| 406 | 16 | 0.8 | 594 | 10 | US-09-864-761-15373 | Sequence 15373, A |
| c 407 | 16 | 0.8 | 608 | 9 | US-09-986-480-54 | Sequence 54, Appl |
| 408 | 16 | 0.8 | 611 | 10 | US-09-770-149-863 | Sequence 863, App |
| 409 | 16 | 0.8 | 620 | 10 | US-09-728-446-628 | Sequence 628, App |
| c 410 | 16 | 0.8 | 648 | 10 | US-09-747-155-30 | Sequence 30, Appl |
| 411 | 16 | 0.8 | 654 | 9 | US-09-938-842A-2648 | Sequence 2648, Ap |
| c 412 | 16 | 0.8 | 697 | 10 | US-09-770-149-278 | Sequence 278, App |
| 413 | 16 | 0.8 | 699 | 10 | US-09-770-149-266 | Sequence 266, App |
| 414 | 16 | 0.8 | 708 | 12 | US-10-044-090-400 | Sequence 400, App |
| c 415 | 16 | 0.8 | 749 | 10 | US-09-910-943-174 | Sequence 174, App |
| 416 | 16 | 0.8 | 764 | 10 | US-09-770-445-941 | Sequence 941, App |
| 417 | 16 | 0.8 | 807 | 9 | US-09-938-842A-212 | Sequence 212, App |
| c 418 | 16 | 0.8 | 810 | 9 | US-09-938-842A-1361 | Sequence 1361, Ap |
| 419 | 16 | 0.8 | 843 | 9 | US-09-938-842A-2300 | Sequence 2300, Ap |
| c 420 | 16 | 0.8 | 845 | 10 | US-09-452-599-25 | Sequence 25, Appl |
| c 421 | 16 | 0.8 | 893 | 9 | US-09-938-842A-3623 | Sequence 3623, Ap |
| c 422 | 16 | 0.8 | 915 | 10 | US-09-764-864-471 | Sequence 471, App |
| c 423 | 16 | 0.8 | 917 | 10 | US-09-833-381-1582 | Sequence 1582, Ap |
| c 424 | 16 | 0.8 | 925 | 10 | US-09-969-708-116 | Sequence 116, App |
| 425 | 16 | 0.8 | 928 | 9 | US-10-259-520-1 | Sequence 1, Appli |
| 426 | 16 | 0.8 | 928 | 10 | US-09-263-811-1 | Sequence 1, Appli |
| 427 | 16 | 0.8 | 958 | 10 | US-09-880-107-2206 | Sequence 2206, Ap |
| 428 | 16 | 0.8 | 960 | 10 | US-09-886-055-70 | Sequence 70, Appl |
| 429 | 16 | 0.8 | 968 | 9 | US-09-938-842A-4479 | Sequence 4479, Ap |
| 430 | 16 | 0.8 | 1050 | 9 | US-09-976-736-77 | Sequence 77, Appl |
| 431 | 16 | 0.8 | 1068 | 10 | US-09-731-872-156 | Sequence 156, App |
| c 432 | 16 | 0.8 | 1072 | 10 | US-09-770-445-131 | Sequence 131, App |
| c 433 | 16 | 0.8 | 1082 | 10 | US-09-925-301-441 | Sequence 441, App |
| 434 | 16 | 0.8 | 1089 | 10 | US-09-886-055-182 | Sequence 182, App |
| c 435 | 16 | 0.8 | 1095 | 10 | US-09-939-980-129 | Sequence 129, App |
| 436 | 16 | 0.8 | 1148 | 10 | US-09-925-300-184 | Sequence 184, App |
| c 437 | 16 | 0.8 | 1152 | 10 | US-09-765-205-43 | Sequence 43, Appl |
| c 438 | 16 | 0.8 | 1154 | 10 | US-09-867-550-1491 | Sequence 1491, Ap |
| c 439 | 16 | 0.8 | 1159 | 10 | US-09-925-300-516 | Sequence 516, App |
| c 440 | 16 | 0.8 | 1168 | 9 | US-10-008-118A-23 | Sequence 23, Appl |
| c 441 | 16 | 0.8 | 1168 | 10 | US-09-443-704-23 | Sequence 23, Appl |
| 442 | 16 | 0.8 | 1175 | 9 | US-10-051-307-4 | Sequence 4, Appli |
| 443 | 16 | 0.8 | 1175 | 9 | US-09-822-846-212 | Sequence 212, App |
| c 444 | 16 | 0.8 | 1194 | 10 | US-09-815-242-7897 | Sequence 7897, Ap |
| c 445 | 16 | 0.8 | 1194 | 10 | US-09-815-242-7904 | Sequence 7904, Ap |
| 446 | 16 | 0.8 | 1200 | 10 | US-09-887-576-708 | Sequence 708, App |
| c 447 | 16 | 0.8 | 1200 | 10 | US-09-887-576-737 | Sequence 737, App |
| 448 | 16 | 0.8 | 1206 | 9 | US-09-938-842A-3112 | Sequence 3112, Ap |
| 449 | 16 | 0.8 | 1247 | 10 | US-09-801-574-74 | Sequence 74, Appl |
| 450 | 16 | 0.8 | 1250 | 9 | US-10-098-841-164 | Sequence 164, App |
| 451 | 16 | 0.8 | 1308 | 10 | US-09-815-242-7927 | Sequence 7927, Ap |
| 452 | 16 | 0.8 | 1309 | 10 | US-09-925-297-189 | Sequence 189, App |
| 453 | 16 | 0.8 | 1362 | 9 | US-09-738-626-2749 | Sequence 2749, Ap |
| 454 | 16 | 0.8 | 1383 | 10 | US-09-801-574-71 | Sequence 71, Appl |
| 455 | 16 | 0.8 | 1385 | 9 | US-09-764-868-486 | Sequence 486, App |
| c 456 | 16 | 0.8 | 1410 | 10 | US-09-801-368-181 | Sequence 181, App |
| c 457 | 16 | 0.8 | 1415 | 10 | US-09-867-550-1521 | Sequence 1521, Ap |
| c 458 | 16 | 0.8 | 1475 | 10 | US-09-925-302-216 | Sequence 216, App |
| c 459 | 16 | 0.8 | 1496 | 10 | US-09-969-347-201 | Sequence 201, App |
| 460 | 16 | 0.8 | 1507 | 10 | US-09-801-574-86 | Sequence 86, Appl |
| 461 | 16 | 0.8 | 1515 | 9 | US-10-014-162-108 | Sequence 108, App |
| 462 | 16 | 0.8 | 1521 | 10 | US-09-801-368-213 | Sequence 213, App |
| 463 | 16 | 0.8 | 1549 | 9 | US-10-001-835-102 | Sequence 102, App |
| 464 | 16 | 0.8 | 1584 | 9 | US-09-854-133-392 | Sequence 392, App |
| 465 | 16 | 0.8 | 1584 | 10 | US-09-738-973-392 | Sequence 392, App |
| c 466 | 16 | 0.8 | 1586 | 9 | US-09-938-842A-3746 | Sequence 3746, Ap |
| c 467 | 16 | 0.8 | 1594 | 10 | US-09-840-787-61 | Sequence 61, Appl |
| c 468 | 16 | 0.8 | 1606 | 10 | US-09-853-386-55 | Sequence 55, Appl |
| c 469 | 16 | 0.8 | 1607 | 9 | US-10-121-235-5 | Sequence 5, Appli |
| c 470 | 16 | 0.8 | 1620 | 9 | US-09-860-670-75 | Sequence 75, Appl |
| c 471 | 16 | 0.8 | 1642 | 10 | US-09-925-301-452 | Sequence 452, App |
| 472 | 16 | 0.8 | 1662 | 9 | US-09-938-842A-1014 | Sequence 1014, Ap |
| 473 | 16 | 0.8 | 1686 | 10 | US-09-833-381-2019 | Sequence 2019, Ap |
| c 474 | 16 | 0.8 | 1709 | 9 | US-09-895-913A-117 | Sequence 117, App |
| c 475 | 16 | 0.8 | 1712 | 10 | US-09-764-887-629 | Sequence 629, App |
| 476 | 16 | 0.8 | 1715 | 9 | US-10-152-661-437 | Sequence 437, App |
| 477 | 16 | 0.8 | 1729 | 9 | US-10-152-661-68 | Sequence 68, Appl |
| 478 | 16 | 0.8 | 1748 | 10 | US-09-801-574-73 | Sequence 73, Appl |
| 479 | 16 | 0.8 | 1752 | 10 | US-09-815-242-3958 | Sequence 3958, Ap |
| 480 | 16 | 0.8 | 1770 | 10 | US-09-815-242-6781 | Sequence 6781, Ap |
| 481 | 16 | 0.8 | 1790 | 12 | US-10-044-090-505 | Sequence 505, App |
| c 482 | 16 | 0.8 | 1799 | 10 | US-09-764-877-3615 | Sequence 3615, Ap |
| 483 | 16 | 0.8 | 1808 | 10 | US-09-822-849A-311 | Sequence 311, App |
| 484 | 16 | 0.8 | 1817 | 10 | US-09-924-417-64 | Sequence 64, Appl |
| c 485 | 16 | 0.8 | 1818 | 9 | US-09-981-876-87 | Sequence 87, Appl |
| c 486 | 16 | 0.8 | 1818 | 9 | US-09-148-545-87 | Sequence 87, Appl |
| 487 | 16 | 0.8 | 1824 | 12 | US-10-044-090-372 | Sequence 372, App |
| c 488 | 16 | 0.8 | 1852 | 10 | US-09-969-852-4 | Sequence 4, Appli |
| 489 | 16 | 0.8 | 1855 | 9 | US-10-000-512-5 | Sequence 5, Appli |
| 490 | 16 | 0.8 | 1869 | 9 | US-10-028-072-269 | Sequence 269, App |
| 491 | 16 | 0.8 | 1869 | 9 | US-10-121-049-269 | Sequence 269, App |
| 492 | 16 | 0.8 | 1869 | 9 | US-10-123-904-269 | Sequence 269, App |
| 493 | 16 | 0.8 | 1869 | 9 | US-10-140-470-269 | Sequence 269, App |
| 494 | 16 | 0.8 | 1869 | 9 | US-10-175-746-269 | Sequence 269, App |
| 495 | 16 | 0.8 | 1869 | 9 | US-10-176-918-269 | Sequence 269, App |
| 496 | 16 | 0.8 | 1869 | 9 | US-10-176-921-269 | Sequence 269, App |
| 497 | 16 | 0.8 | 1869 | 9 | US-10-137-865-269 | Sequence 269, App |
| 498 | 16 | 0.8 | 1869 | 9 | US-10-140-474-269 | Sequence 269, App |
| 499 | 16 | 0.8 | 1882 | 10 | US-09-917-800A-1536 | Sequence 1536, Ap |
| c 500 | 16 | 0.8 | 1890 | 9 | US-09-764-868-372 | Sequence 372, App |
| c 501 | 16 | 0.8 | 1899 | 9 | US-09-938-842A-4384 | Sequence 4384, Ap |
| 502 | 16 | 0.8 | 1911 | 9 | US-09-938-842A-3533 | Sequence 3533, Ap |
| c 503 | 16 | 0.8 | 1918 | 9 | US-09-860-670-77 | Sequence 77, Appl |
| 504 | 16 | 0.8 | 1925 | 9 | US-09-981-876-86 | Sequence 86, Appl |
| 505 | 16 | 0.8 | 1925 | 9 | US-09-148-545-86 | Sequence 86, Appl |
| 506 | 16 | 0.8 | 1926 | 9 | US-09-981-876-21 | Sequence 21, Appl |
| 507 | 16 | 0.8 | 1926 | 9 | US-10-024-632-5 | Sequence 5, Appli |
| 508 | 16 | 0.8 | 1926 | 9 | US-09-148-545-21 | Sequence 21, Appl |
| 509 | 16 | 0.8 | 1926 | 12 | US-10-044-090-28 | Sequence 28, Appl |
| c 510 | 16 | 0.8 | 1941 | 9 | US-10-098-841-61 | Sequence 61, Appl |
| 511 | 16 | 0.8 | 1943 | 10 | US-09-864-761-5096 | Sequence 5096, Ap |
| 512 | 16 | 0.8 | 1971 | 10 | US-09-764-869-2384 | Sequence 2384, Ap |
| 513 | 16 | 0.8 | 1971 | 10 | US-09-764-869-2385 | Sequence 2385, Ap |
| 514 | 16 | 0.8 | 1971 | 10 | US-09-764-869-2386 | Sequence 2386, Ap |
| 515 | 16 | 0.8 | 1971 | 10 | US-09-764-847-1569 | Sequence 1569, Ap |
| 516 | 16 | 0.8 | 1971 | 10 | US-09-764-847-1570 | Sequence 1570, Ap |
| 517 | 16 | 0.8 | 1971 | 10 | US-09-764-847-1571 | Sequence 1571, Ap |
| c 518 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-2757 | Sequence 2757, Ap |
| c 519 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-3246 | Sequence 3246, Ap |
| c 520 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-3635 | Sequence 3635, Ap |
| 521 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-3794 | Sequence 3794, Ap |
| 522 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-4005 | Sequence 4005, Ap |
| 523 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-4218 | Sequence 4218, Ap |
| 524 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-4287 | Sequence 4287, Ap |
| c 525 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-4550 | Sequence 4550, Ap |
| 526 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-4652 | Sequence 4652, Ap |
| c 527 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-4854 | Sequence 4854, Ap |
| 528 | 16 | 0.8 | 2000 | 9 | US-09-938-842A-5147 | Sequence 5147, Ap |
| c 529 | 16 | 0.8 | 2035 | 10 | US-09-850-351A-10 | Sequence 10, Appl |
| 530 | 16 | 0.8 | 2048 | 9 | US-09-902-941-1924 | Sequence 1924, Ap |

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|---|---|---|---|---|---|---|
| | 531 | 16 | 0.8 | 2048 | 9 | US-09-849-626-1924 | Sequence 1924, Ap |
| | 532 | 16 | 0.8 | 2051 | 10 | US-09-954-456-1180 | Sequence 1180, Ap |
| c | 533 | 16 | 0.8 | 2084 | 10 | US-09-822-849A-267 | Sequence 267, App |
| c | 534 | 16 | 0.8 | 2090 | 10 | US-09-764-847-1842 | Sequence 1842, Ap |
| c | 535 | 16 | 0.8 | 2091 | 10 | US-09-764-847-1843 | Sequence 1843, Ap |
| c | 536 | 16 | 0.8 | 2128 | 9 | US-10-152-661-487 | Sequence 487, App |
| c | 537 | 16 | 0.8 | 2157 | 10 | US-09-729-674-131 | Sequence 131, App |
| c | 538 | 16 | 0.8 | 2230 | 9 | US-10-161-510-2 | Sequence 2, Appli |
| c | 539 | 16 | 0.8 | 2233 | 10 | US-09-817-913-10 | Sequence 10, Appl |
| c | 540 | 16 | 0.8 | 2233 | 10 | US-09-817-538-10 | Sequence 10, Appl |
| | 541 | 16 | 0.8 | 2235 | 10 | US-09-822-849A-378 | Sequence 378, App |
| c | 542 | 16 | 0.8 | 2256 | 10 | US-09-899-471-1 | Sequence 1, Appli |
| c | 543 | 16 | 0.8 | 2328 | 10 | US-09-899-471-4 | Sequence 4, Appli |
| c | 544 | 16 | 0.8 | 2337 | 9 | US-09-759-130B-202 | Sequence 202, App |
| c | 545 | 16 | 0.8 | 2350 | 10 | US-09-070-927A-109 | Sequence 109, App |
| c | 546 | 16 | 0.8 | 2407 | 10 | US-09-765-994-1 | Sequence 1, Appli |
| c | 547 | 16 | 0.8 | 2448 | 9 | US-09-759-130B-215 | Sequence 215, App |
| c | 548 | 16 | 0.8 | 2456 | 9 | US-09-764-868-437 | Sequence 437, App |
| c | 549 | 16 | 0.8 | 2460 | 10 | US-09-894-993-1 | Sequence 1, Appli |
| | 550 | 16 | 0.8 | 2481 | 10 | US-09-764-864-124 | Sequence 124, App |
| | 551 | 16 | 0.8 | 2493 | 9 | US-09-764-868-63 | Sequence 63, Appl |
| c | 552 | 16 | 0.8 | 2493 | 10 | US-09-764-887-628 | Sequence 628, App |
| | 553 | 16 | 0.8 | 2494 | 9 | US-09-822-846-238 | Sequence 238, App |
| c | 554 | 16 | 0.8 | 2594 | 9 | US-10-028-072-245 | Sequence 245, App |
| c | 555 | 16 | 0.8 | 2594 | 9 | US-10-121-049-245 | Sequence 245, App |
| c | 556 | 16 | 0.8 | 2594 | 9 | US-10-123-904-245 | Sequence 245, App |
| c | 557 | 16 | 0.8 | 2594 | 9 | US-10-140-470-245 | Sequence 245, App |
| c | 558 | 16 | 0.8 | 2594 | 9 | US-10-175-746-245 | Sequence 245, App |
| c | 559 | 16 | 0.8 | 2594 | 9 | US-10-176-918-245 | Sequence 245, App |
| c | 560 | 16 | 0.8 | 2594 | 9 | US-10-176-921-245 | Sequence 245, App |
| c | 561 | 16 | 0.8 | 2594 | 9 | US-10-137-865-245 | Sequence 245, App |
| c | 562 | 16 | 0.8 | 2594 | 9 | US-10-140-474-245 | Sequence 245, App |
| | 563 | 16 | 0.8 | 2660 | 10 | US-09-864-864-339 | Sequence 339, App |
| | 564 | 16 | 0.8 | 2674 | 10 | US-09-917-800A-1500 | Sequence 1500, Ap |
| | 565 | 16 | 0.8 | 2690 | 10 | US-09-833-790-420 | Sequence 420, App |
| | 566 | 16 | 0.8 | 2697 | 10 | US-09-960-253-149 | Sequence 149, App |
| | 567 | 16 | 0.8 | 2755 | 12 | US-10-044-090-496 | Sequence 496, App |
| c | 568 | 16 | 0.8 | 2818 | 9 | US-10-121-235-7 | Sequence 7, Appli |
| | 569 | 16 | 0.8 | 2831 | 10 | US-09-822-830A-195 | Sequence 195, App |
| | 570 | 16 | 0.8 | 2893 | 10 | US-09-905-846-1 | Sequence 1, Appli |
| c | 571 | 16 | 0.8 | 2896 | 9 | US-09-949-842-11 | Sequence 11, Appl |
| | 572 | 16 | 0.8 | 2956 | 10 | US-09-764-870-620 | Sequence 620, App |
| c | 573 | 16 | 0.8 | 2966 | 9 | US-09-981-353-33 | Sequence 33, Appl |
| c | 574 | 16 | 0.8 | 2974 | 9 | US-10-174-590-521 | Sequence 521, App |
| c | 575 | 16 | 0.8 | 2974 | 9 | US-10-176-758-521 | Sequence 521, App |
| c | 576 | 16 | 0.8 | 2974 | 9 | US-10-175-737-521 | Sequence 521, App |
| c | 577 | 16 | 0.8 | 2974 | 9 | US-10-173-706-521 | Sequence 521, App |
| c | 578 | 16 | 0.8 | 2974 | 9 | US-10-175-738-521 | Sequence 521, App |
| c | 579 | 16 | 0.8 | 2974 | 9 | US-10-175-752-521 | Sequence 521, App |
| c | 580 | 16 | 0.8 | 2974 | 9 | US-10-176-482-521 | Sequence 521, App |
| c | 581 | 16 | 0.8 | 2974 | 9 | US-10-176-757-521 | Sequence 521, App |
| c | 582 | 16 | 0.8 | 2974 | 9 | US-10-176-913-521 | Sequence 521, App |
| c | 583 | 16 | 0.8 | 2974 | 9 | US-10-180-552-521 | Sequence 521, App |
| c | 584 | 16 | 0.8 | 2974 | 9 | US-10-180-557-521 | Sequence 521, App |
| c | 585 | 16 | 0.8 | 2974 | 9 | US-10-173-700-521 | Sequence 521, App |
| c | 586 | 16 | 0.8 | 2974 | 9 | US-10-174-572-521 | Sequence 521, App |
| c | 587 | 16 | 0.8 | 2974 | 9 | US-10-174-579-521 | Sequence 521, App |
| c | 588 | 16 | 0.8 | 2974 | 9 | US-10-174-582-521 | Sequence 521, App |
| c | 589 | 16 | 0.8 | 2974 | 9 | US-10-174-588-521 | Sequence 521, App |
| c | 590 | 16 | 0.8 | 2974 | 9 | US-10-175-739-521 | Sequence 521, App |
| c | 591 | 16 | 0.8 | 2974 | 9 | US-10-175-740-521 | Sequence 521, App |
| c | 592 | 16 | 0.8 | 2974 | 9 | US-10-175-743-521 | Sequence 521, App |
| c | 593 | 16 | 0.8 | 2974 | 9 | US-10-176-488-521 | Sequence 521, App |
| c | 594 | 16 | 0.8 | 2974 | 9 | US-10-176-492-521 | Sequence 521, App |
| c | 595 | 16 | 0.8 | 2974 | 9 | US-10-176-747-521 | Sequence 521, App |
| c | 596 | 16 | 0.8 | 2974 | 9 | US-10-176-750-521 | Sequence 521, App |
| c | 597 | 16 | 0.8 | 2974 | 9 | US-10-176-985-521 | Sequence 521, App |
| c | 598 | 16 | 0.8 | 2974 | 9 | US-10-176-987-521 | Sequence 521, App |
| c | 599 | 16 | 0.8 | 2974 | 9 | US-10-176-991-521 | Sequence 521, App |
| c | 600 | 16 | 0.8 | 2974 | 9 | US-10-176-992-521 | Sequence 521, App |
| c | 601 | 16 | 0.8 | 2974 | 9 | US-10-176-993-521 | Sequence 521, App |
| c | 602 | 16 | 0.8 | 2974 | 9 | US-10-184-658-521 | Sequence 521, App |
| c | 603 | 16 | 0.8 | 2974 | 9 | US-10-173-695-521 | Sequence 521, App |
| c | 604 | 16 | 0.8 | 2974 | 9 | US-10-173-697-521 | Sequence 521, App |
| c | 605 | 16 | 0.8 | 2974 | 9 | US-10-173-705-521 | Sequence 521, App |
| c | 606 | 16 | 0.8 | 2974 | 9 | US-10-174-576-521 | Sequence 521, App |
| c | 607 | 16 | 0.8 | 2974 | 9 | US-10-174-585-521 | Sequence 521, App |
| c | 608 | 16 | 0.8 | 2974 | 9 | US-10-174-586-521 | Sequence 521, App |
| c | 609 | 16 | 0.8 | 2974 | 9 | US-10-175-747-521 | Sequence 521, App |
| c | 610 | 16 | 0.8 | 2974 | 9 | US-10-176-481-521 | Sequence 521, App |
| c | 611 | 16 | 0.8 | 2974 | 9 | US-10-176-485-521 | Sequence 521, App |
| c | 612 | 16 | 0.8 | 2974 | 9 | US-10-176-487-521 | Sequence 521, App |
| c | 613 | 16 | 0.8 | 2974 | 9 | US-10-176-493-521 | Sequence 521, App |
| c | 614 | 16 | 0.8 | 2974 | 9 | US-10-176-756-521 | Sequence 521, App |
| c | 615 | 16 | 0.8 | 2974 | 9 | US-10-176-911-521 | Sequence 521, App |
| c | 616 | 16 | 0.8 | 2974 | 9 | US-10-176-919-521 | Sequence 521, App |
| c | 617 | 16 | 0.8 | 2974 | 9 | US-10-176-925-521 | Sequence 521, App |
| c | 618 | 16 | 0.8 | 2974 | 9 | US-10-176-978-521 | Sequence 521, App |
| c | 619 | 16 | 0.8 | 2974 | 9 | US-10-179-510-521 | Sequence 521, App |
| c | 620 | 16 | 0.8 | 2974 | 9 | US-10-180-543-521 | Sequence 521, App |
| c | 621 | 16 | 0.8 | 2974 | 9 | US-10-180-544-521 | Sequence 521, App |
| c | 622 | 16 | 0.8 | 2974 | 9 | US-10-180-546-521 | Sequence 521, App |
| c | 623 | 16 | 0.8 | 2974 | 9 | US-10-180-547-521 | Sequence 521, App |
| c | 624 | 16 | 0.8 | 2974 | 9 | US-10-180-549-521 | Sequence 521, App |
| c | 625 | 16 | 0.8 | 2974 | 9 | US-10-180-555-521 | Sequence 521, App |
| c | 626 | 16 | 0.8 | 2974 | 9 | US-10-180-559-521 | Sequence 521, App |
| c | 627 | 16 | 0.8 | 2974 | 9 | US-10-181-000-521 | Sequence 521, App |
| c | 628 | 16 | 0.8 | 2974 | 9 | US-10-183-010-521 | Sequence 521, App |
| c | 629 | 16 | 0.8 | 2974 | 9 | US-10-183-012-521 | Sequence 521, App |
| c | 630 | 16 | 0.8 | 2974 | 9 | US-10-184-614-521 | Sequence 521, App |
| c | 631 | 16 | 0.8 | 2974 | 9 | US-10-184-623-521 | Sequence 521, App |
| c | 632 | 16 | 0.8 | 2974 | 9 | US-10-184-635-521 | Sequence 521, App |
| c | 633 | 16 | 0.8 | 2974 | 9 | US-10-184-637-521 | Sequence 521, App |
| c | 634 | 16 | 0.8 | 2974 | 9 | US-10-184-646-521 | Sequence 521, App |
| c | 635 | 16 | 0.8 | 2974 | 9 | US-10-184-647-521 | Sequence 521, App |
| c | 636 | 16 | 0.8 | 2974 | 9 | US-10-184-652-521 | Sequence 521, App |
| c | 637 | 16 | 0.8 | 2974 | 9 | US-10-187-594-521 | Sequence 521, App |
| c | 638 | 16 | 0.8 | 2974 | 9 | US-10-187-596-521 | Sequence 521, App |
| c | 639 | 16 | 0.8 | 2974 | 9 | US-10-187-745-521 | Sequence 521, App |
| c | 640 | 16 | 0.8 | 2974 | 9 | US-10-187-885-521 | Sequence 521, App |
| c | 641 | 16 | 0.8 | 2974 | 9 | US-10-187-886-521 | Sequence 521, App |
| c | 642 | 16 | 0.8 | 2974 | 9 | US-10-199-464-521 | Sequence 521, App |
| c | 643 | 16 | 0.8 | 2974 | 12 | US-10-052-586-521 | Sequence 521, App |
| | 644 | 16 | 0.8 | 2975 | 10 | US-09-905-846-5 | Sequence 5, Appli |
| c | 645 | 16 | 0.8 | 3006 | 9 | US-09-962-678-1 | Sequence 1, Appli |
| c | 646 | 16 | 0.8 | 3042 | 9 | US-10-161-510-3 | Sequence 3, Appli |
| c | 647 | 16 | 0.8 | 3096 | 9 | US-09-822-846-113 | Sequence 113, App |
| c | 648 | 16 | 0.8 | 3098 | 9 | US-10-098-841-15 | Sequence 15, Appl |
| | 649 | 16 | 0.8 | 3109 | 10 | US-09-925-301-544 | Sequence 544, App |
| c | 650 | 16 | 0.8 | 3112 | 9 | US-09-822-846-112 | Sequence 112, App |
| c | 651 | 16 | 0.8 | 3178 | 9 | US-10-108-605-124 | Sequence 124, App |
| c | 652 | 16 | 0.8 | 3178 | 9 | US-10-108-605-128 | Sequence 128, App |
| | 653 | 16 | 0.8 | 3184 | 9 | US-10-108-605-324 | Sequence 324, App |
| | 654 | 16 | 0.8 | 3260 | 10 | US-09-808-701-10 | Sequence 10, Appl |
| | 655 | 16 | 0.8 | 3375 | 9 | US-09-938-842A-667 | Sequence 667, App |
| | 656 | 16 | 0.8 | 3517 | 10 | US-09-925-302-182 | Sequence 182, App |
| | 657 | 16 | 0.8 | 3545 | 10 | US-09-764-864-144 | Sequence 144, App |
| | 658 | 16 | 0.8 | 3564 | 9 | US-09-938-842A-582 | Sequence 582, App |
| c | 659 | 16 | 0.8 | 3572 | 10 | US-09-925-302-280 | Sequence 280, App |
| | 660 | 16 | 0.8 | 3725 | 9 | US-10-002-344A-12 | Sequence 12, Appl |
| c | 661 | 16 | 0.8 | 3747 | 9 | US-10-071-766-33 | Sequence 33, Appl |
| c | 662 | 16 | 0.8 | 3770 | 9 | US-09-759-130B-201 | Sequence 201, App |
| c | 663 | 16 | 0.8 | 3927 | 10 | US-09-974-300-2642 | Sequence 2642, Ap |
| | 664 | 16 | 0.8 | 3936 | 10 | US-09-919-172-49 | Sequence 49, Appl |
| | 665 | 16 | 0.8 | 3937 | 9 | US-09-989-920-161 | Sequence 161, App |
| | 666 | 16 | 0.8 | 3954 | 9 | US-10-071-766-44 | Sequence 44, Appl |
| | 667 | 16 | 0.8 | 3996 | 12 | US-10-147-268-3 | Sequence 3, Appli |
| | 668 | 16 | 0.8 | 4176 | 10 | US-09-070-927A-188 | Sequence 188, App |
| c | 669 | 16 | 0.8 | 4185 | 9 | US-10-026-188-1 | Sequence 1, Appli |
| c | 670 | 16 | 0.8 | 4237 | 10 | US-09-745-763-20 | Sequence 20, Appl |
| | 671 | 16 | 0.8 | 4409 | 9 | US-09-874-162A-7 | Sequence 7, Appli |
| | 672 | 16 | 0.8 | 4441 | 9 | US-09-874-162A-4 | Sequence 4, Appli |
| | 673 | 16 | 0.8 | 4441 | 10 | US-09-796-348-20 | Sequence 20, Appl |
| | 674 | 16 | 0.8 | 4441 | 10 | US-09-969-347-169 | Sequence 169, App |
| | 675 | 16 | 0.8 | 4779 | 10 | US-09-764-878-216 | Sequence 216, App |
| | 676 | 16 | 0.8 | 4810 | 10 | US-09-885-329-5 | Sequence 5, Appli |

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| | 677 | 16 | 0.8 | 5055 | 10 | US-09-764-855-311 |
| c | 678 | 16 | 0.8 | 5115 | 10 | US-09-853-386-57 |
| | 679 | 16 | 0.8 | 5139 | 10 | US-09-764-869-1894 |
| c | 680 | 16 | 0.8 | 5476 | 10 | US-09-764-864-1790 |
| c | 681 | 16 | 0.8 | 5476 | 10 | US-09-764-864-1791 |
| c | 682 | 16 | 0.8 | 5476 | 10 | US-09-764-877-2811 |
| c | 683 | 16 | 0.8 | 5476 | 10 | US-09-764-877-2812 |
| | 684 | 16 | 0.8 | 5814 | 10 | US-09-764-847-1860 |
| | 685 | 16 | 0.8 | 5869 | 10 | US-09-880-107-3839 |
| | 686 | 16 | 0.8 | 5929 | 9 | US-10-071-766-133 |
| c | 687 | 16 | 0.8 | 6092 | 10 | US-09-070-927A-225 |
| c | 688 | 16 | 0.8 | 6152 | 9 | US-09-742-096-1 |
| | 689 | 16 | 0.8 | 6476 | 9 | US-09-854-133-428 |
| | 690 | 16 | 0.8 | 6476 | 10 | US-09-738-973-428 |
| c | 691 | 16 | 0.8 | 6531 | 10 | US-09-070-927A-75 |
| | 692 | 16 | 0.8 | 6691 | 10 | US-09-070-927A-88 |
| c | 693 | 16 | 0.8 | 6777 | 12 | US-10-044-090-289 |
| | 694 | 16 | 0.8 | 6784 | 10 | US-09-764-855-312 |
| c | 695 | 16 | 0.8 | 6837 | 9 | US-09-928-847B-49 |
| | 696 | 16 | 0.8 | 7215 | 10 | US-09-070-927A-102 |
| | 697 | 16 | 0.8 | 7287 | 10 | US-09-070-927A-210 |
| | 698 | 16 | 0.8 | 7596 | 10 | US-09-728-952-1 |
| c | 699 | 16 | 0.8 | 7770 | 10 | US-09-991-630-23 |
| | 700 | 16 | 0.8 | 7964 | 10 | US-09-070-927A-101 |
| c | 701 | 16 | 0.8 | 8136 | 10 | US-09-764-870-589 |
| c | 702 | 16 | 0.8 | 8180 | 10 | US-09-905-129-8 |
| c | 703 | 16 | 0.8 | 8180 | 10 | US-09-991-630-8 |
| c | 704 | 16 | 0.8 | 8262 | 10 | US-09-905-129-6 |
| c | 705 | 16 | 0.8 | 8262 | 10 | US-09-991-630-6 |
| c | 706 | 16 | 0.8 | 8495 | 9 | US-10-108-605-356 |
| | 707 | 16 | 0.8 | 8918 | 10 | US-09-764-864-1682 |
| | 708 | 16 | 0.8 | 8919 | 10 | US-09-764-864-1683 |
| c | 709 | 16 | 0.8 | 9717 | 10 | US-09-764-847-1581 |
| | 710 | 16 | 0.8 | 10503 | 10 | US-09-764-870-579 |
| c | 711 | 16 | 0.8 | 10503 | 10 | US-09-764-853-854 |
| c | 712 | 16 | 0.8 | 10503 | 10 | US-09-764-860-1032 |
| c | 713 | 16 | 0.8 | 11792 | 9 | US-09-764-868-1396 |
| c | 714 | 16 | 0.8 | 11792 | 9 | US-09-764-868-1397 |
| c | 715 | 16 | 0.8 | 11879 | 10 | US-09-070-927A-181 |
| c | 716 | 16 | 0.8 | 12822 | 10 | US-09-764-847-1579 |
| c | 717 | 16 | 0.8 | 13048 | 10 | US-09-880-107-2364 |
| c | 718 | 16 | 0.8 | 13953 | 9 | US-10-096-961-3 |
| | 719 | 16 | 0.8 | 13957 | 10 | US-09-782-378A-22 |
| | 720 | 16 | 0.8 | 13957 | 10 | US-09-880-107-2284 |
| | 721 | 16 | 0.8 | 14176 | 10 | US-09-764-864-1644 |
| c | 722 | 16 | 0.8 | 14176 | 10 | US-09-764-864-1644 |
| | 723 | 16 | 0.8 | 14417 | 9 | US-09-860-670-251 |
| | 724 | 16 | 0.8 | 14426 | 9 | US-09-860-670-249 |
| | 725 | 16 | 0.8 | 14426 | 9 | US-09-860-670-252 |
| | 726 | 16 | 0.8 | 14448 | 9 | US-09-860-670-250 |
| | 727 | 16 | 0.8 | 14451 | 9 | US-09-860-670-253 |
| c | 728 | 16 | 0.8 | 14698 | 9 | US-09-764-868-1429 |
| c | 729 | 16 | 0.8 | 15231 | 10 | US-09-917-800A-1505 |
| | 730 | 16 | 0.8 | 15295 | 10 | US-09-764-877-3404 |
| c | 731 | 16 | 0.8 | 16086 | 10 | US-09-764-877-2385 |
| | 732 | 16 | 0.8 | 17203 | 10 | US-09-864-761-20867 |
| | 733 | 16 | 0.8 | 17704 | 10 | US-09-764-847-1865 |
| | 734 | 16 | 0.8 | 17707 | 10 | US-09-764-847-1864 |
| c | 735 | 16 | 0.8 | 17849 | 10 | US-09-764-847-1315 |
| c | 736 | 16 | 0.8 | 17862 | 10 | US-09-764-847-1313 |
| | 737 | 16 | 0.8 | 21636 | 10 | US-09-416-384A-3 |
| c | 738 | 16 | 0.8 | 25165 | 9 | US-10-114-170-39 |
| | 739 | 16 | 0.8 | 28588 | 10 | US-09-764-887-399 |
| | 740 | 16 | 0.8 | 32042 | 9 | US-10-118-984-44 |
| | 741 | 16 | 0.8 | 32042 | 10 | US-09-728-721-63 |
| c | 742 | 16 | 0.8 | 32134 | 10 | US-09-764-847-1057 |
| c | 743 | 16 | 0.8 | 32134 | 10 | US-09-764-877-3535 |
| | 744 | 16 | 0.8 | 32152 | 10 | US-09-764-855-328 |
| c | 745 | 16 | 0.8 | 32191 | 10 | US-09-764-877-3374 |
| | 746 | 16 | 0.8 | 32192 | 10 | US-09-764-877-3657 |
| | 747 | 16 | 0.8 | 32204 | 10 | US-09-764-855-327 |
| | 748 | 16 | 0.8 | 32207 | 10 | US-09-764-877-3250 |
| | 749 | 16 | 0.8 | 33239 | 10 | US-09-814-950-3 |

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| Sequence 311, App |
| Sequence 57, Appl |
| Sequence 1894, Ap |
| Sequence 1790, Ap |
| Sequence 1791, Ap |
| Sequence 2811, Ap |
| Sequence 2812, Ap |
| Sequence 1860, Ap |
| Sequence 3839, Ap |
| Sequence 133, App |
| Sequence 225, App |
| Sequence 1, Appli |
| Sequence 428, App |
| Sequence 428, App |
| Sequence 75, Appl |
| Sequence 88, Appl |
| Sequence 289, App |
| Sequence 312, App |
| Sequence 49, Appl |
| Sequence 102, App |
| Sequence 210, App |
| Sequence 1, Appli |
| Sequence 23, Appl |
| Sequence 101, App |
| Sequence 589, App |
| Sequence 8, Appli |
| Sequence 8, Appli |
| Sequence 6, Appli |
| Sequence 6, Appli |
| Sequence 356, App |
| Sequence 1682, Ap |
| Sequence 1683, Ap |
| Sequence 1581, Ap |
| Sequence 579, App |
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| Sequence 3535, Ap |
| Sequence 328, App |
| Sequence 3374, Ap |
| Sequence 3657, Ap |
| Sequence 327, App |
| Sequence 3250, Ap |
| Sequence 3, Appli |

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| | 751 | 16 | 0.8 | 62804 | 12 | US-10-096-960-3 |
| c | 752 | 16 | 0.8 | 65042 | 9 | US-10-229-124-3 |
| | 753 | 16 | 0.8 | 81940 | 9 | US-09-759-508B-1 |
| | 754 | 16 | 0.8 | 126512 | 10 | US-09-804-474A-3 |
| | 755 | 16 | 0.8 | 133893 | 9 | US-10-161-510-1 |
| c | 756 | 16 | 0.8 | 148567 | 9 | US-10-254-869-3 |
| c | 757 | 16 | 0.8 | 148567 | 10 | US-09-801-876B-3 |
| c | 758 | 16 | 0.8 | 152331 | 9 | US-10-095-407-16 |
| | 759 | 16 | 0.8 | 155074 | 9 | US-10-026-188-6 |
| c | 760 | 16 | 0.8 | 155074 | 9 | US-10-026-188-6 |
| c | 761 | 16 | 0.8 | 173808 | 12 | US-10-003-806-10 |
| c | 762 | 16 | 0.8 | 180557 | 12 | US-10-003-806-6 |
| c | 763 | 16 | 0.8 | 180557 | 12 | US-10-003-806-9 |
| c | 764 | 16 | 0.8 | 186957 | 9 | US-10-185-770-3 |
| | 765 | 16 | 0.8 | 197496 | 9 | US-09-877-177-10 |
| c | 766 | 16 | 0.8 | 197496 | 9 | US-09-877-177-10 |
| c | 767 | 16 | 0.8 | 302250 | 10 | US-09-962-832-154 |
| | 768 | 16 | 0.8 | 326014 | 10 | US-09-731-231A-3 |
| c | 769 | 16 | 0.8 | 368004 | 10 | US-09-949-654-3 |
| c | 770 | 16 | 0.8 | 397658 | 10 | US-09-813-320-3 |
| | 771 | 16 | 0.8 | 465237 | 10 | US-09-933-267A-1 |
| c | 772 | 16 | 0.8 | 465237 | 10 | US-09-933-267A-1 |
| c | 773 | 16 | 0.8 | 513509 | 9 | US-09-754-853A-4 |
| | 774 | 16 | 0.8 | 640681 | 10 | US-09-790-988-1 |
| c | 775 | 16 | 0.8 | 640681 | 10 | US-09-790-988-1 |
| c | 776 | 16 | 0.8 | 659158 | 9 | US-09-771-208-20 |
| | 777 | 16 | 0.8 | 1503841 | 9 | US-09-946-807-1 |
| c | 778 | 16 | 0.8 | 1503841 | 9 | US-09-946-807-1 |
| | 779 | 16 | 0.8 | 1503841 | 10 | US-09-795-668-1 |
| c | 780 | 16 | 0.8 | 1503841 | 10 | US-09-795-668-1 |
| | 781 | 16 | 0.8 | 1503841 | 10 | US-09-795-686-1 |
| c | 782 | 16 | 0.8 | 1503841 | 10 | US-09-795-686-1 |
| | 783 | 15 | 0.7 | 17 | 10 | US-09-866-108-9900 |
| | 784 | 15 | 0.7 | 17 | 10 | US-09-866-108-9901 |
| | 785 | 15 | 0.7 | 17 | 10 | US-09-866-108-9902 |
| | 786 | 15 | 0.7 | 18 | 9 | US-09-885-297A-14 |
| | 787 | 15 | 0.7 | 25 | 10 | US-09-866-108-14792 |
| | 788 | 15 | 0.7 | 25 | 10 | US-09-866-108-14793 |
| | 789 | 15 | 0.7 | 25 | 10 | US-09-866-108-14794 |
| | 790 | 15 | 0.7 | 25 | 10 | US-09-866-108-14795 |
| | 791 | 15 | 0.7 | 25 | 10 | US-09-866-108-14796 |
| | 792 | 15 | 0.7 | 25 | 10 | US-09-866-108-14797 |
| | 793 | 15 | 0.7 | 25 | 10 | US-09-866-108-14798 |
| | 794 | 15 | 0.7 | 25 | 10 | US-09-866-108-14799 |
| | 795 | 15 | 0.7 | 25 | 10 | US-09-866-108-14800 |
| | 796 | 15 | 0.7 | 25 | 10 | US-09-866-108-14801 |
| | 797 | 15 | 0.7 | 25 | 10 | US-09-866-108-14802 |
| c | 798 | 15 | 0.7 | 45 | 10 | US-09-765-272-235 |
| | 799 | 15 | 0.7 | 60 | 9 | US-10-219-248-22 |
| | 800 | 15 | 0.7 | 60 | 9 | US-10-219-247-22 |
| | 801 | 15 | 0.7 | 60 | 10 | US-09-855-722-22 |
| | 802 | 15 | 0.7 | 69 | 10 | US-09-785-632A-62 |
| | 803 | 15 | 0.7 | 69 | 10 | US-09-785-632A-110 |
| c | 804 | 15 | 0.7 | 76 | 10 | US-09-983-965-5771 |
| c | 805 | 15 | 0.7 | 78 | 10 | US-09-974-300-6950 |
| c | 806 | 15 | 0.7 | 90 | 9 | US-09-736-457-1288 |
| c | 807 | 15 | 0.7 | 90 | 9 | US-09-902-941-1288 |
| c | 808 | 15 | 0.7 | 90 | 9 | US-09-849-626-1288 |
| c | 809 | 15 | 0.7 | 100 | 10 | US-09-728-446-609 |
| | 810 | 15 | 0.7 | 102 | 10 | US-09-974-300-629 |
| c | 811 | 15 | 0.7 | 105 | 10 | US-09-864-761-29358 |
| c | 812 | 15 | 0.7 | 110 | 10 | US-09-864-761-20411 |
| | 813 | 15 | 0.7 | 111 | 10 | US-09-969-373-1283 |
| | 814 | 15 | 0.7 | 112 | 10 | US-09-864-761-22958 |
| c | 815 | 15 | 0.7 | 115 | 10 | US-09-969-373-1180 |
| c | 816 | 15 | 0.7 | 118 | 10 | US-09-983-965-2194 |
| | 817 | 15 | 0.7 | 122 | 10 | US-09-969-373-1046 |
| c | 818 | 15 | 0.7 | 126 | 10 | US-09-867-701-6967 |
| | 819 | 15 | 0.7 | 127 | 10 | US-09-969-373-811 |
| c | 820 | 15 | 0.7 | 131 | 10 | US-09-563-817-524 |
| | 821 | 15 | 0.7 | 133 | 10 | US-09-924-035A-659 |
| c | 822 | 15 | 0.7 | 136 | 10 | US-09-983-965-1621 |

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| Sequence 3, Appli |
| Sequence 3, Appli |
| Sequence 3, Appli |
| Sequence 1, Appli |
| Sequence 3, Appli |
| Sequence 1, Appli |
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| Sequence 3, Appli |
| Sequence 16, Appl |
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| Sequence 6, Appli |
| Sequence 10, Appl |
| Sequence 6, Appli |
| Sequence 9, Appli |
| Sequence 3, Appli |
| Sequence 10, Appl |
| Sequence 10, Appl |
| Sequence 154, App |
| Sequence 3, Appli |
| Sequence 3, Appli |
| Sequence 3, Appli |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 4, Appli |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 20, Appl |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 1, Appli |
| Sequence 9900, Ap |
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| Sequence 9902, Ap |
| Sequence 14, Appl |
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| Sequence 14793, A |
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| Sequence 14795, A |
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| Sequence 14797, A |
| Sequence 14798, A |
| Sequence 14799, A |
| Sequence 14800, A |
| Sequence 14801, A |
| Sequence 14802, A |
| Sequence 235, App |
| Sequence 22, Appl |
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| Sequence 22, Appl |
| Sequence 62, Appl |
| Sequence 110, App |
| Sequence 5771, Ap |
| Sequence 6950, Ap |
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| Sequence 629, App |
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| Sequence 2194, Ap |
| Sequence 1046, Ap |
| Sequence 6967, Ap |
| Sequence 811, App |
| Sequence 524, App |
| Sequence 659, App |
| Sequence 1621, Ap |

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| c | 823 | 15 | 0.7 | 139 | 10 | US-09-867-701-1053 Sequence 1053, Ap |
| | 824 | 15 | 0.7 | 150 | 10 | US-09-864-761-32408 Sequence 32408, A |
| c | 825 | 15 | 0.7 | 157 | 10 | US-09-864-761-31915 Sequence 31915, A |
| | 826 | 15 | 0.7 | 162 | 10 | US-09-864-761-24104 Sequence 24104, A |
| c | 827 | 15 | 0.7 | 176 | 10 | US-09-878-574-12625 Sequence 12625, A |
| c | 828 | 15 | 0.7 | 181 | 10 | US-09-919-580-192 Sequence 192, App |
| | 829 | 15 | 0.7 | 183 | 10 | US-09-867-701-6012 Sequence 6012, Ap |
| c | 830 | 15 | 0.7 | 190 | 10 | US-09-783-590-7200 Sequence 7200, Ap |
| c | 831 | 15 | 0.7 | 190 | 10 | US-09-925-300-876 Sequence 876, App |
| c | 832 | 15 | 0.7 | 191 | 10 | US-09-917-800A-599 Sequence 599, App |
| | 833 | 15 | 0.7 | 192 | 9 | US-09-738-626-327 Sequence 327, App |
| c | 834 | 15 | 0.7 | 193 | 10 | US-09-969-373-529 Sequence 529, App |
| | 835 | 15 | 0.7 | 195 | 10 | US-09-864-761-19176 Sequence 19176, A |
| c | 836 | 15 | 0.7 | 196 | 9 | US-10-025-380-849 Sequence 849, App |
| | 837 | 15 | 0.7 | 196 | 10 | US-09-923-876-4350 Sequence 4350, Ap |
| c | 838 | 15 | 0.7 | 196 | 10 | US-09-922-217-849 Sequence 849, App |
| c | 839 | 15 | 0.7 | 196 | 10 | US-09-833-263-849 Sequence 849, App |
| c | 840 | 15 | 0.7 | 201 | 10 | US-09-960-352-5181 Sequence 5181, Ap |
| | 841 | 15 | 0.7 | 201 | 10 | US-09-960-352-7478 Sequence 7478, Ap |
| | 842 | 15 | 0.7 | 203 | 9 | US-09-754-853A-387 Sequence 387, App |
| c | 843 | 15 | 0.7 | 204 | 9 | US-09-796-692-6431 Sequence 6431, Ap |
| | 844 | 15 | 0.7 | 206 | 10 | US-09-867-701-3555 Sequence 3555, Ap |
| c | 845 | 15 | 0.7 | 208 | 9 | US-09-796-692-9479 Sequence 9479, Ap |
| c | 846 | 15 | 0.7 | 213 | 10 | US-09-294-093B-5858 Sequence 5858, Ap |
| | 847 | 15 | 0.7 | 216 | 10 | US-09-815-242-3026 Sequence 3026, Ap |
| | 848 | 15 | 0.7 | 217 | 10 | US-09-864-761-20168 Sequence 20168, A |
| c | 849 | 15 | 0.7 | 220 | 10 | US-09-878-574-11970 Sequence 11970, A |
| | 850 | 15 | 0.7 | 222 | 10 | US-09-783-590-5257 Sequence 5257, Ap |
| c | 851 | 15 | 0.7 | 227 | 10 | US-09-876-889-76 Sequence 76, Appl |
| | 852 | 15 | 0.7 | 228 | 9 | US-09-933-797-686 Sequence 686, App |
| c | 853 | 15 | 0.7 | 230 | 10 | US-09-960-352-8496 Sequence 8496, Ap |
| | 854 | 15 | 0.7 | 230 | 10 | US-09-998-598-2187 Sequence 2187, Ap |
| | 855 | 15 | 0.7 | 236 | 10 | US-09-960-352-5865 Sequence 5865, Ap |
| c | 856 | 15 | 0.7 | 240 | 10 | US-09-960-352-1500 Sequence 1500, Ap |
| | 857 | 15 | 0.7 | 242 | 10 | US-09-783-590-9629 Sequence 9629, Ap |
| | 858 | 15 | 0.7 | 246 | 10 | US-09-878-574-8013 Sequence 8013, Ap |
| c | 859 | 15 | 0.7 | 248 | 10 | US-09-878-574-13902 Sequence 13902, A |
| | 860 | 15 | 0.7 | 248 | 10 | US-09-969-373-729 Sequence 729, App |
| c | 861 | 15 | 0.7 | 251 | 10 | US-09-878-574-13993 Sequence 13993, A |
| c | 862 | 15 | 0.7 | 252 | 10 | US-09-923-876-1960 Sequence 1960, Ap |
| | 863 | 15 | 0.7 | 254 | 10 | US-09-878-574-6300 Sequence 6300, Ap |
| c | 864 | 15 | 0.7 | 255 | 10 | US-09-728-446-541 Sequence 541, App |
| | 865 | 15 | 0.7 | 257 | 10 | US-09-783-590-3087 Sequence 3087, Ap |
| c | 866 | 15 | 0.7 | 258 | 10 | US-09-878-574-7053 Sequence 7053, Ap |
| | 867 | 15 | 0.7 | 261 | 9 | US-09-796-692-3883 Sequence 3883, Ap |
| c | 868 | 15 | 0.7 | 261 | 9 | US-10-015-219-1329 Sequence 1329, Ap |
| | 869 | 15 | 0.7 | 261 | 9 | US-10-015-219-1564 Sequence 1564, Ap |
| c | 870 | 15 | 0.7 | 261 | 10 | US-09-777-564-1329 Sequence 1329, Ap |
| | 871 | 15 | 0.7 | 261 | 10 | US-09-777-564-1564 Sequence 1564, Ap |
| c | 872 | 15 | 0.7 | 262 | 10 | US-09-864-761-28337 Sequence 28337, A |
| | 873 | 15 | 0.7 | 262 | 10 | US-09-878-574-10542 Sequence 10542, A |
| | 874 | 15 | 0.7 | 263 | 9 | US-09-754-853A-159 Sequence 159, App |
| c | 875 | 15 | 0.7 | 265 | 10 | US-09-867-550-209 Sequence 209, App |
| c | 876 | 15 | 0.7 | 265 | 10 | US-09-878-574-14057 Sequence 14057, A |
| | 877 | 15 | 0.7 | 265 | 10 | US-09-867-701-8985 Sequence 8985, Ap |
| | 878 | 15 | 0.7 | 266 | 10 | US-09-294-093B-808 Sequence 808, App |
| c | 879 | 15 | 0.7 | 266 | 10 | US-09-878-574-15109 Sequence 15109, A |
| c | 880 | 15 | 0.7 | 267 | 9 | US-09-736-457-115 Sequence 115, App |
| c | 881 | 15 | 0.7 | 267 | 9 | US-09-902-941-115 Sequence 115, App |
| c | 882 | 15 | 0.7 | 267 | 9 | US-09-849-626-115 Sequence 115, App |
| | 883 | 15 | 0.7 | 268 | 10 | US-09-848-889-4 Sequence 4, Appli |
| c | 884 | 15 | 0.7 | 268 | 10 | US-09-864-761-25533 Sequence 25533, A |
| c | 885 | 15 | 0.7 | 268 | 10 | US-09-878-574-8702 Sequence 8702, Ap |
| | 886 | 15 | 0.7 | 270 | 9 | US-10-079-623-62 Sequence 62, Appl |
| c | 887 | 15 | 0.7 | 271 | 9 | US-10-040-739-379 Sequence 379, App |
| c | 888 | 15 | 0.7 | 275 | 9 | US-09-736-457-1243 Sequence 1243, Ap |
| c | 889 | 15 | 0.7 | 275 | 9 | US-09-902-941-1243 Sequence 1243, Ap |
| c | 890 | 15 | 0.7 | 275 | 9 | US-09-849-626-1243 Sequence 1243, Ap |
| | 891 | 15 | 0.7 | 275 | 10 | US-09-878-574-13629 Sequence 13629, A |
| c | 892 | 15 | 0.7 | 280 | 10 | US-09-983-965-2601 Sequence 2601, Ap |
| c | 893 | 15 | 0.7 | 282 | 10 | US-09-263-689-28 Sequence 28, Appl |
| | 894 | 15 | 0.7 | 284 | 10 | US-09-294-093B-1570 Sequence 1570, Ap |
| c | 895 | 15 | 0.7 | 285 | 10 | US-09-864-761-20299 Sequence 20299, A |
| c | 896 | 15 | 0.7 | 285 | 10 | US-09-878-574-13175 Sequence 13175, A |
| c | 897 | 15 | 0.7 | 286 | 10 | US-09-294-093B-920 Sequence 920, App |
| | 898 | 15 | 0.7 | 286 | 10 | US-09-878-574-14696 Sequence 14696, A |
| | 899 | 15 | 0.7 | 287 | 9 | US-09-796-692-6400 Sequence 6400, Ap |
| | 900 | 15 | 0.7 | 287 | 9 | US-09-796-692-6513 Sequence 6513, Ap |
| | 901 | 15 | 0.7 | 287 | 9 | US-09-796-692-6651 Sequence 6651, Ap |
| c | 902 | 15 | 0.7 | 287 | 10 | US-09-864-761-25758 Sequence 25758, A |
| c | 903 | 15 | 0.7 | 288 | 10 | US-09-983-965-1067 Sequence 1067, Ap |
| c | 904 | 15 | 0.7 | 291 | 10 | US-09-764-847-165 Sequence 165, App |
| c | 905 | 15 | 0.7 | 291 | 10 | US-09-764-847-1264 Sequence 1264, Ap |
| c | 906 | 15 | 0.7 | 291 | 10 | US-09-764-847-1265 Sequence 1265, Ap |
| c | 907 | 15 | 0.7 | 291 | 10 | US-09-764-847-1266 Sequence 1266, Ap |
| c | 908 | 15 | 0.7 | 292 | 10 | US-09-880-107-3228 Sequence 3228, Ap |
| | 909 | 15 | 0.7 | 293 | 10 | US-09-867-701-3543 Sequence 3543, Ap |
| c | 910 | 15 | 0.7 | 294 | 10 | US-09-294-093B-1124 Sequence 1124, Ap |
| c | 911 | 15 | 0.7 | 294 | 10 | US-09-815-343-177 Sequence 177, App |
| c | 912 | 15 | 0.7 | 294 | 10 | US-09-815-242-4630 Sequence 4630, Ap |
| | 913 | 15 | 0.7 | 294 | 10 | US-09-867-701-9114 Sequence 9114, Ap |
| c | 914 | 15 | 0.7 | 295 | 10 | US-09-294-093B-5333 Sequence 5333, Ap |
| | 915 | 15 | 0.7 | 299 | 10 | US-09-867-701-10376 Sequence 10376, A |
| c | 916 | 15 | 0.7 | 300 | 9 | US-09-975-719-198 Sequence 198, App |
| | 917 | 15 | 0.7 | 300 | 10 | US-09-841-132-528 Sequence 528, App |
| | 918 | 15 | 0.7 | 301 | 9 | US-09-232-880-249 Sequence 249, App |
| | 919 | 15 | 0.7 | 301 | 9 | US-10-012-896-249 Sequence 249, App |
| | 920 | 15 | 0.7 | 301 | 9 | US-09-895-793-249 Sequence 249, App |
| | 921 | 15 | 0.7 | 301 | 9 | US-09-895-814-249 Sequence 249, App |
| | 922 | 15 | 0.7 | 301 | 10 | US-09-759-143-249 Sequence 249, App |
| | 923 | 15 | 0.7 | 301 | 10 | US-09-780-669-249 Sequence 249, App |
| | 924 | 15 | 0.7 | 301 | 10 | US-09-822-827-249 Sequence 249, App |
| c | 925 | 15 | 0.7 | 303 | 10 | US-09-878-574-621 Sequence 621, App |
| | 926 | 15 | 0.7 | 307 | 10 | US-09-867-701-9108 Sequence 9108, Ap |
| | 927 | 15 | 0.7 | 311 | 10 | US-09-960-352-8358 Sequence 8358, Ap |
| | 928 | 15 | 0.7 | 312 | 10 | US-09-878-574-381 Sequence 381, App |
| c | 929 | 15 | 0.7 | 314 | 9 | US-09-954-531-634 Sequence 634, App |
| | 930 | 15 | 0.7 | 315 | 9 | US-10-025-380-412 Sequence 412, App |
| | 931 | 15 | 0.7 | 315 | 10 | US-09-922-217-412 Sequence 412, App |
| | 932 | 15 | 0.7 | 315 | 10 | US-09-833-263-412 Sequence 412, App |
| c | 933 | 15 | 0.7 | 315 | 10 | US-09-878-574-15286 Sequence 15286, A |
| | 934 | 15 | 0.7 | 317 | 10 | US-09-728-446-38 Sequence 38, Appl |
| c | 935 | 15 | 0.7 | 317 | 10 | US-09-960-352-9141 Sequence 9141, Ap |
| c | 936 | 15 | 0.7 | 320 | 10 | US-09-969-373-1406 Sequence 1406, Ap |
| c | 937 | 15 | 0.7 | 320 | 10 | US-09-960-352-2839 Sequence 2839, Ap |
| c | 938 | 15 | 0.7 | 321 | 10 | US-09-815-242-6985 Sequence 6985, Ap |
| c | 939 | 15 | 0.7 | 322 | 9 | US-10-025-380-224 Sequence 224, App |
| c | 940 | 15 | 0.7 | 322 | 10 | US-09-922-217-224 Sequence 224, App |
| c | 941 | 15 | 0.7 | 322 | 10 | US-09-728-446-926 Sequence 926, App |
| c | 942 | 15 | 0.7 | 322 | 10 | US-09-833-263-224 Sequence 224, App |
| | 943 | 15 | 0.7 | 324 | 10 | US-09-878-574-31 Sequence 31, Appl |
| c | 944 | 15 | 0.7 | 324 | 10 | US-09-954-456-1039 Sequence 1039, Ap |
| | 945 | 15 | 0.7 | 326 | 10 | US-09-728-446-218 Sequence 218, App |
| c | 946 | 15 | 0.7 | 328 | 9 | US-09-736-457-231 Sequence 231, App |
| c | 947 | 15 | 0.7 | 328 | 9 | US-09-902-941-231 Sequence 231, App |
| c | 948 | 15 | 0.7 | 328 | 9 | US-09-849-626-231 Sequence 231, App |
| c | 949 | 15 | 0.7 | 328 | 10 | US-09-834-975-482 Sequence 482, App |
| | 950 | 15 | 0.7 | 330 | 10 | US-09-867-701-9021 Sequence 9021, Ap |
| | 951 | 15 | 0.7 | 332 | 10 | US-09-815-242-2451 Sequence 2451, Ap |
| c | 952 | 15 | 0.7 | 332 | 10 | US-09-867-701-4378 Sequence 4378, Ap |
| | 953 | 15 | 0.7 | 332 | 10 | US-09-764-864-613 Sequence 613, App |
| | 954 | 15 | 0.7 | 332 | 10 | US-09-983-965-5260 Sequence 5260, Ap |
| c | 955 | 15 | 0.7 | 333 | 10 | US-09-815-242-8324 Sequence 8324, Ap |
| c | 956 | 15 | 0.7 | 333 | 10 | US-09-783-590-12349 Sequence 12349, A |
| | 957 | 15 | 0.7 | 335 | 10 | US-09-864-761-18428 Sequence 18428, A |
| | 958 | 15 | 0.7 | 338 | 10 | US-09-969-373-260 Sequence 260, App |
| c | 959 | 15 | 0.7 | 338 | 10 | US-09-969-373-260 Sequence 260, App |
| | 960 | 15 | 0.7 | 339 | 9 | US-09-975-719-258 Sequence 258, App |
| c | 961 | 15 | 0.7 | 343 | 10 | US-09-969-708-89 Sequence 89, Appl |
| c | 962 | 15 | 0.7 | 343 | 10 | US-09-969-708-620 Sequence 620, App |
| | 963 | 15 | 0.7 | 343 | 10 | US-09-783-590-1808 Sequence 1808, Ap |
| c | 964 | 15 | 0.7 | 343 | 10 | US-09-880-107-2136 Sequence 2136, Ap |
| | 965 | 15 | 0.7 | 346 | 10 | US-09-867-701-7707 Sequence 7707, Ap |
| | 966 | 15 | 0.7 | 347 | 9 | US-09-796-692-2812 Sequence 2812, Ap |
| c | 967 | 15 | 0.7 | 348 | 10 | US-09-960-352-9542 Sequence 9542, Ap |
| | 968 | 15 | 0.7 | 350 | 9 | US-09-796-692-4607 Sequence 4607, Ap |

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| c 969 | 15 | 0.7 | 350 | 10 | US-09-770-791-701 | Sequence 701, App |
| 970 | 15 | 0.7 | 351 | 10 | US-09-867-701-854 | Sequence 854, App |
| c 971 | 15 | 0.7 | 352 | 10 | US-09-969-373-344 | Sequence 344, App |
| c 972 | 15 | 0.7 | 352 | 10 | US-09-960-352-10129 | Sequence 10129, A |
| 973 | 15 | 0.7 | 353 | 10 | US-09-764-847-137 | Sequence 137, App |
| c 974 | 15 | 0.7 | 354 | 10 | US-09-764-877-382 | Sequence 382, App |
| c 975 | 15 | 0.7 | 356 | 10 | US-09-960-352-12579 | Sequence 12579, A |
| 976 | 15 | 0.7 | 363 | 9 | US-10-001-883-44 | Sequence 44, Appl |
| c 977 | 15 | 0.7 | 364 | 9 | US-10-040-739-288 | Sequence 288, App |
| 978 | 15 | 0.7 | 364 | 10 | US-09-960-352-9419 | Sequence 9419, Ap |
| 979 | 15 | 0.7 | 365 | 10 | US-09-878-574-1860 | Sequence 1860, Ap |
| 980 | 15 | 0.7 | 365 | 10 | US-09-867-701-1277 | Sequence 1277, Ap |
| c 981 | 15 | 0.7 | 365 | 10 | US-09-960-352-12014 | Sequence 12014, A |
| 982 | 15 | 0.7 | 366 | 9 | US-09-933-797-499 | Sequence 499, App |
| 983 | 15 | 0.7 | 366 | 10 | US-09-974-300-5559 | Sequence 5559, Ap |
| c 984 | 15 | 0.7 | 368 | 10 | US-09-802-669-97 | Sequence 97, Appl |
| c 985 | 15 | 0.7 | 368 | 10 | US-09-783-590-10931 | Sequence 10931, A |
| 986 | 15 | 0.7 | 368 | 10 | US-09-764-877-318 | Sequence 318, App |
| 987 | 15 | 0.7 | 370 | 10 | US-09-867-701-245 | Sequence 245, App |
| c 988 | 15 | 0.7 | 370 | 10 | US-09-867-701-245 | Sequence 245, App |
| 989 | 15 | 0.7 | 370 | 10 | US-09-960-352-11540 | Sequence 11540, A |
| 990 | 15 | 0.7 | 372 | 9 | US-09-860-670-38 | Sequence 38, Appl |
| 991 | 15 | 0.7 | 372 | 10 | US-09-764-869-170 | Sequence 170, App |
| 992 | 15 | 0.7 | 373 | 10 | US-09-864-761-18695 | Sequence 18695, A |
| 993 | 15 | 0.7 | 374 | 9 | US-09-796-692-4261 | Sequence 4261, Ap |
| 994 | 15 | 0.7 | 374 | 10 | US-09-867-550-1833 | Sequence 1833, Ap |
| c 995 | 15 | 0.7 | 375 | 10 | US-09-764-869-253 | Sequence 253, App |
| 996 | 15 | 0.7 | 375 | 10 | US-09-878-574-2165 | Sequence 2165, Ap |
| c 997 | 15 | 0.7 | 378 | 9 | US-09-975-719-197 | Sequence 197, App |
| c 998 | 15 | 0.7 | 378 | 10 | US-09-878-574-3225 | Sequence 3225, Ap |
| c 999 | 15 | 0.7 | 378 | 10 | US-09-960-352-602 | Sequence 602, App |
| c1000 | 15 | 0.7 | 379 | 10 | US-09-864-761-19500 | Sequence 19500, A |

ALIGNMENTS

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RESULT 1
US-09-954-456-539
; Sequence 539, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 539
;   LENGTH: 2102
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-539

  Query Match           100.0%;  Score 2102;  DB 10;  Length 2102;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
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Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
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Qy   2101 GT 2102
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Db   2101 GT 2102
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RESULT 2
US-09-765-231A-6
; Sequence 6, Application US/09765231A
; Patent No. US20020119452A1
; GENERAL INFORMATION:
;  APPLICANT: Searle/Monsanto
;  APPLICANT:  Phippard, Deborah
;  APPLICANT:  Vasanthakamur, Geetha
;  APPLICANT:  Dotson, Stanton
;  APPLICANT:  Ma, Xiao-Jun
;  TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
;  TITLE OF INVENTION:  vectors, and cells
;  FILE REFERENCE: SO-3221 PR
;  CURRENT APPLICATION NUMBER: US/09/765,231A
;  CURRENT FILING DATE:  2001-01-18
;  NUMBER OF SEQ ID NOS: 82
; SEQ ID NO 6
;   LENGTH: 2263
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: 1-2263
;   LOCATION: unknown
;   OTHER INFORMATION: unsure at all n locations
US-09-765-231A-6

  Query Match             93.6%;  Score 1968;  DB 10;  Length 2263;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2088;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;
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Qy      15 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 74
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Db     161 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 220

Qy      75 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 134
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Db     221 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 280

Qy     135 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 194
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Db   1061 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1120

Qy    974 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1033
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Qy   1034 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1093
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Qy   1094 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1153
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Db   1541 ATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCC 1600

Qy   1454 TTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGA 1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1601 TTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGA 1660

Qy   1514 AAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGG 1573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1661 AAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGG 1720

Qy   1574 AAATAAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCT 1633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1721 AAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCT 1780

Qy   1634 CTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAA 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   1781 CTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAA 1840

Qy   1694 GGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAA 1753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1841 GGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAA 1900

Qy   1754 CCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGT 1813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1901 CCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGT 1960

Qy   1814 TGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTA 1873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1961 TGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTA 2020

Qy   1874 AAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATC 1933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2021 AAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATC 2080

Qy   1934 GAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATT 1993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2081 GAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATT 2140

Qy   1994 TATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGA 2053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2141 TATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGA 2200

Qy   2054 AGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2102
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   2201 AGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2249


RESULT 3
US-09-964-824A-446/c
; Sequence 446, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
;  APPLICANT: Horrigan, Stephen
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-73
;  CURRENT APPLICATION NUMBER: US/09/964,824A
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: US/60/236,033
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,032
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US/60/236,028
;  PRIOR FILING DATE: 2000-09-28
;  NUMBER OF SEQ ID NOS: 583
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 446
;   LENGTH: 586
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-964-824A-446

  Query Match             13.3%;  Score 279;  DB 10;  Length 586;
  Best Local Similarity   99.5%;  Pred. No. 1.7e-129;
  Matches  379;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    934 CCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCT 993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    426 CCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCT 367

Qy    994 CACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGA 1053
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    366 CACCAACTTTTCAGAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGA 307

Qy   1054 GTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTG 1113
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    306 GTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTG 247

Qy   1114 GAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTT 1173
```

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     246 GAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTCACGTTGACAGGTT 187

Qy    1174 TGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAA 1233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     186 TGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAA 127

Qy    1234 ATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAA 1293
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     126 ATACACCCAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGCATATTGGATAAAA 67

Qy    1294 TAAATGCAATTGTGCTCTTCA 1314
              |||||||||||||||||||||
Db      66 TAAATGCAATTGTGCTCTTCA 46


RESULT 4
US-09-867-701-9693
; Sequence 9693, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;  APPLICANT: Aglate, Paul A.
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE:  2001-05-29
;  NUMBER OF SEQ ID NOS: 10912
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9693
;   LENGTH: 368
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(368)
;   OTHER INFORMATION: n = A,T,C or G
US-09-867-701-9693

  Query Match             11.5%;  Score 241;  DB 10;  Length 368;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-110;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       3 GCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGC 62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGC 60

Qy      63 GCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCC 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCC 120

Qy     123 CGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCC 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCC 180

Qy     183 CCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACT 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACT 240

Qy     243 G 243
              |
Db     241 G 241


RESULT 5
US-09-815-343-1286/c
; Sequence 1286, Application US/09815343
; Patent No. US20010055596A1
; GENERAL INFORMATION:
;  APPLICANT: Meagher, Madeleine
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  King, Gordon E.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.504
;  CURRENT APPLICATION NUMBER: US/09/815,343
;  CURRENT FILING DATE:  2001-03-22
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1286
;   LENGTH: 479
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(479)
;   OTHER INFORMATION: n = A,T,C or G
US-09-815-343-1286

  Query Match             11.4%;  Score 240;  DB 10;  Length 479;
  Best Local Similarity   99.5%;  Pred. No. 5.5e-110;
  Matches  410;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     412 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 353

Qy    1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     352 GTCNTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 293

Qy    1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 233

Qy    1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     232 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 173

Qy    1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATC-AAAAGCAAATAAAA 1619
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     172 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAAGCAAATAAAA 113

Qy    1620 ACCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTA 1679
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     112 ACCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTA 53

Qy    1680 ATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTT 1731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      52 ATCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTT 1


RESULT 6
US-10-046-935-1922/c
; Sequence 1922, Application US/10046935
; Patent No. US20020156011A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Stolk, John A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.527C1
;  CURRENT APPLICATION NUMBER: US/10/046,935
;  CURRENT FILING DATE:  2002-01-15
;  NUMBER OF SEQ ID NOS: 2239
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1922
;   LENGTH: 221
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-046-935-1922
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  Query Match             10.5%;  Score 221;  DB 9;  Length 221;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-100;
  Matches  221;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    646 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 162

Qy    706 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 765
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 102

Qy    766 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 825
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 42

Qy    826 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 866
          |||||||||||||||||||||||||||||||||||||||||
Db     41 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 1


RESULT 7
US-09-878-178-1922/c
; Sequence 1922, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Yuqiu
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.527
;  CURRENT APPLICATION NUMBER: US/09/878,178
;  CURRENT FILING DATE:  2001-06-08
;  NUMBER OF SEQ ID NOS: 2237
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1922
;   LENGTH: 221
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-878-178-1922

  Query Match             10.5%;  Score 221;  DB 9;  Length 221;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-100;
  Matches  221;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    646 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 705
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 ACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGA 162

Qy    706 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 765
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 GTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATG 102

Qy    766 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 825
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 GAATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTA 42

Qy    826 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 866
          |||||||||||||||||||||||||||||||||||||||||
Db     41 ATAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGT 1


RESULT 8
US-09-925-299-368
; Sequence 368, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 368
;   LENGTH: 548
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (370)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (378)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (384)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (412)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (429)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (449)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (471)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (490)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (495)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (528)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-368

  Query Match              9.3%;  Score 196;  DB 10;  Length 548;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-88;
  Matches  196;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    849 GAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCT 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      9 GAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCT 68

Qy    909 GAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACA 968
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     69 GAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACA 128

Qy    969 GTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACC 1028
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 GTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACC 188

Qy   1029 ACACCAAATGCTCAAG 1044
          ||||||||||||||||
Db    189 ACACCAAATGCTCAAG 204


RESULT 9
US-09-925-664-26
; Sequence 26, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
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;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 747
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   NAME/KEY: CDS
;   LOCATION: (1)..(744)
;   OTHER INFORMATION:
US-09-925-664-26

  Query Match             5.5%;  Score 115;  DB 9;  Length 747;
  Best Local Similarity   100.0%;  Pred. No. 2e-47;
  Matches  115;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1097 CCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTG 1156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    633 CCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTG 692

Qy   1157 TTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1211
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    693 TTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 747


RESULT 10
US-09-925-664-22
; Sequence 22, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 134
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-925-664-22

  Query Match             5.4%;  Score 114;  DB 9;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-47;
  Matches  114;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1098 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     10 CCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGT 69

Qy   1158 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 1211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 TTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAG 123


RESULT 11
US-09-925-664-23/c
; Sequence 23, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
;  PRIOR APPLICATION NUMBER: 08/761,277
;  PRIOR FILING DATE: 1996-12-06
;  NUMBER OF SEQ ID NOS: 80
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;   TYPE: DNA
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;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-925-664-23

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; Sequence 24, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
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US-09-925-664-24

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RESULT 13
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; Sequence 29, Application US/09925664
; Patent No. US20020160006A1
; GENERAL INFORMATION:
;  APPLICANT: Denney, Jr., Dan W.
;  TITLE OF INVENTION: Methods of Treating Lymphoma and Leukemia
;  FILE REFERENCE: GENITOPE-06499
;  CURRENT APPLICATION NUMBER: US/09/925,664
;  CURRENT FILING DATE:  2001-08-09
;  PRIOR APPLICATION NUMBER: 09/370,453
;  PRIOR FILING DATE: 1999-08-09
;  PRIOR APPLICATION NUMBER: 08/644,664
;  PRIOR FILING DATE: 1996-05-01
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;   LOCATION: (1)..(783)
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; Sequence 36, Application US/09729835
; Patent No. US20010016647A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 29 Human Secreted Proteins
;  FILE REFERENCE: PZ015P1
;  CURRENT APPLICATION NUMBER: US/09/729,835
;  CURRENT FILING DATE:  2000-12-06
;  PRIOR APPLICATION NUMBER: 09/257,179
;  PRIOR FILING DATE: 1999-02-25
;  PRIOR APPLICATION NUMBER: 60/056,270
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;  PRIOR FILING DATE: 1997-08-29
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;  NUMBER OF SEQ ID NOS: 128
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US-09-729-835-36

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RESULT 15
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; Sequence 1, Application US/09799952
; Patent No. US20010023066A1
; GENERAL INFORMATION:
;  APPLICANT: Kinders, Robert J.
;  APPLICANT:  Enfield, David L.
;  APPLICANT:  Hass, Michael
;  TITLE OF INVENTION: METHODS OF SCREENING FOR OR TREATING
;  TITLE OF INVENTION:  CANCERS OR AUTOIMMUNE DISORDERS IN WHICH A COMPLEMENT C3 OR
;  TITLE OF INVENTION:  C3 RELATED PROTEIN IS ASSOCIATED
;  FILE REFERENCE: 130001.405C1
;  CURRENT APPLICATION NUMBER: US/09/799,952
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 22
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US-09-799-952-1

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| c | 154 | 17 | 0.8 | 1354 | 1 | US-08-514-014-9 | Sequence 9, Appli |
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| | 156 | 17 | 0.8 | 1357 | 4 | US-09-560-639-5 | Sequence 5, Appli |
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| | 158 | 17 | 0.8 | 1383 | 3 | US-09-400-742-7 | Sequence 7, Appli |
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| | 165 | 17 | 0.8 | 2058 | 4 | US-09-560-639-4 | Sequence 4, Appli |
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| c | 173 | 17 | 0.8 | 2248 | 4 | US-09-345-214-20 | Sequence 20, Appl |
| | 174 | 17 | 0.8 | 2281 | 4 | US-09-484-970B-103 | Sequence 103, App |
| c | 175 | 17 | 0.8 | 2663 | 1 | US-08-136-743B-3 | Sequence 3, Appli |
| | 176 | 17 | 0.8 | 2883 | 4 | US-09-422-936-44 | Sequence 44, Appl |
| | 177 | 17 | 0.8 | 3232 | 4 | US-08-961-527-144 | Sequence 144, App |
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| | 180 | 17 | 0.8 | 3440 | 5 | PCT-US91-01746-27 | Sequence 27, Appl |
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| c | 191 | 17 | 0.8 | 112132 | 4 | US-09-741-150-3 | Sequence 3, Appli |
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| c | 194 | 17 | 0.8 | 246240 | 2 | US-08-724-394A-22 | Sequence 22, Appl |
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| | 196 | 17 | 0.8 | 4411529 | 4 | US-09-103-840A-1 | Sequence 1, Appli |
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| c | 198 | 16 | 0.8 | 27 | 2 | US-08-951-871-16 | Sequence 16, Appl |
| | 199 | 16 | 0.8 | 30 | 1 | US-08-480-784-77 | Sequence 77, Appl |
| | 200 | 16 | 0.8 | 30 | 1 | US-08-483-553-77 | Sequence 77, Appl |
| | 201 | 16 | 0.8 | 30 | 1 | US-08-487-002-77 | Sequence 77, Appl |
| | 202 | 16 | 0.8 | 30 | 1 | US-08-483-554B-77 | Sequence 77, Appl |
| | 203 | 16 | 0.8 | 30 | 1 | US-08-488-011B-77 | Sequence 77, Appl |
| | 204 | 16 | 0.8 | 30 | 4 | US-08-850-727-77 | Sequence 77, Appl |
| | 205 | 16 | 0.8 | 30 | 5 | PCT-US95-10202-77 | Sequence 77, Appl |
| | 206 | 16 | 0.8 | 30 | 5 | PCT-US95-10203-77 | Sequence 77, Appl |
| | 207 | 16 | 0.8 | 30 | 5 | PCT-US95-10220-77 | Sequence 77, Appl |
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| | 211 | 16 | 0.8 | 93 | 4 | US-08-556-978B-88 | Sequence 88, Appl |
| | 212 | 16 | 0.8 | 139 | 2 | US-08-750-654-3 | Sequence 3, Appli |
| | 213 | 16 | 0.8 | 165 | 1 | US-08-209-747-9 | Sequence 9, Appli |
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| | 222 | 16 | 0.8 | 470 | 1 | US-08-480-784-32 | Sequence 32, Appl |
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| | 229 | 16 | 0.8 | 470 | 5 | PCT-US95-10203-32 | Sequence 32, Appl |
| | 230 | 16 | 0.8 | 470 | 5 | PCT-US95-10220-32 | Sequence 32, Appl |
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| | 261 | 16 | 0.8 | 1300 | 4 | US-08-795-876-36 Sequence 36, Appl |
| c | 262 | 16 | 0.8 | 1300 | 4 | US-08-795-876-37 Sequence 37, Appl |
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| 935 | 15 | 0.7 | 3012 | 1 | US-08-454-464-1 | Sequence 1, Appli |
| 936 | 15 | 0.7 | 3012 | 1 | US-08-453-222-1 | Sequence 1, Appli |
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| 963 | 15 | 0.7 | 3390 | 1 | US-08-453-222-26 | Sequence 26, Appl |
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| 977 | 15 | 0.7 | 3480 | 1 | US-08-362-577C-11 | Sequence 11, Appl |
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| 982 | 15 | 0.7 | 3510 | 4 | US-08-961-527-53 | Sequence 53, Appl |
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| c 984 | 15 | 0.7 | 3531 | 1 | US-07-828-788A-7 | Sequence 7, Appli |
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| c 986 | 15 | 0.7 | 3531 | 5 | PCT-US92-11337-7 | Sequence 7, Appli |
| c 987 | 15 | 0.7 | 3531 | 6 | 5169629-1 | Patent No. 5169629 |
| c 988 | 15 | 0.7 | 3534 | 2 | US-08-841-178-24 | Sequence 24, Appl |
| c 989 | 15 | 0.7 | 3534 | 2 | US-08-841-178-25 | Sequence 25, Appl |
| c 990 | 15 | 0.7 | 3534 | 2 | US-08-841-178-26 | Sequence 26, Appl |
| c 991 | 15 | 0.7 | 3537 | 1 | US-08-377-690-3 | Sequence 3, Appli |
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| c 993 | 15 | 0.7 | 3546 | 4 | US-09-118-442-14 | Sequence 14, Appl |
| c 994 | 15 | 0.7 | 3546 | 4 | US-09-118-442-15 | Sequence 15, Appl |
| c 995 | 15 | 0.7 | 3546 | 4 | US-09-677-064-14 | Sequence 14, Appl |
| c 996 | 15 | 0.7 | 3546 | 4 | US-09-677-064-15 | Sequence 15, Appl |
| c 997 | 15 | 0.7 | 3571 | 3 | US-09-280-799-132 | Sequence 132, App |
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| 1000 | 15 | 0.7 | 3588 | 1 | US-07-792-885A-2 | Sequence 2, Appli |

ALIGNMENTS

```
RESULT 1
US-07-811-048-9
; Sequence 9, Application US/07811048
; Patent No. 5264357
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    TITLE OF INVENTION:  Nucleic Acid and Methods for the Synthesis of No. 5264357el Fu
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/811,048
;      FILING DATE:  19911219
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/738171
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/859107
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US86/01177
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/083757
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Robert H.
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  330p1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1489
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2116 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-811-048-9

  Query Match             82.7%;  Score 1739;  DB 1;  Length 2116;
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Db    2038 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2097

Qy    2101 GT 2102
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Db    2098 GT 2099


RESULT 2
US-08-087-007-2
; Sequence 2, Application US/08087007
; Patent No. 5705732
; Patent No. 5705732 5684223
;  GENERAL INFORMATION:
;    APPLICANT:  Sims, Peter J.
;    APPLICANT:  Bothwell, Alfred L.M.
;    APPLICANT:  Elliott, Eileen A.
;    APPLICANT:  Flavell, Richard A.
;    APPLICANT:  Madri, Joseph
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Squinto, Stephen
;    TITLE OF INVENTION:  Universal Donor Cells
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kilpatrick & Cody
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/087,007
;      FILING DATE:  19930701
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  OMRF135
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-815-6500
;      TELEFAX:  404-815-6555
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2847 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank HUMDAF; HUMDAFC1
;      CLONE:  Human DAF cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..819
;      OTHER INFORMATION:  /note= "HUMDAFC1 (Promotor and 5'
;      OTHER INFORMATION:  end of Exon 1, genomic sequence)"
US-08-087-007-2

  Query Match             59.7%;  Score 1255;  DB 1;  Length 2847;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1405;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db    751 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 810

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db    931 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 990

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Db    991 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 1050

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Db   1051 TGACCTGCCTTAAGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 1110

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Db   1111 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 1170

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Db   1651 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 1710

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Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
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Db   1771 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1830

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Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
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RESULT 3
US-08-483-433-2
; Sequence 2, Application US/08483433
; Patent No. 6100443
;  GENERAL INFORMATION:
;    APPLICANT:  Sims et al.
;    TITLE OF INVENTION:  Universal Donor Cells
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,433
;      FILING DATE:
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/087,007
;      FILING DATE:  July 1, 1993
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/906,394
;      FILING DATE:  June 29, 1992
;      CLASSIFICATION:  800
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  OMRF135cip2 div
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-873-8794
;      TELEFAX:  404-873-9794
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2847 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
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;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank HUMDAF; HUMDAFC1
;      CLONE:  Human DAF cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..819
;      OTHER INFORMATION:  /note= "HUMDAFC1 (Promotor and 5'
;      OTHER INFORMATION:  end of Exon 1, genomic sequence)"
US-08-483-433-2

  Query Match             59.7%;  Score 1255;  DB 3;  Length 2847;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1405;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db    751 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 810

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db    811 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 870

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db    871 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 930

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RESULT 4
PCT-US92-05920-2
; Sequence 2, Application PC/TUS9205920
;  GENERAL INFORMATION:
;    APPLICANT:  Sims, Peter J.
;    APPLICANT:  Bothwell, Alfred L.M.
;    APPLICANT:  Elliott, Eileen A.
;    APPLICANT:  Flavell, Richard A.
;    APPLICANT:  Madri, Joseph
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Bell, Leonard
;    APPLICANT:  Squinto, Stephen
;    TITLE OF INVENTION:  Universal Donor Cells
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kilpatrick & Cody
;      STREET:  1100 Peachtree Street, Suite 2800
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  U.S.
;      ZIP:  30309-4530
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US92/05920
;      FILING DATE:  19920714
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  OMRF135
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  404-815-6500
;       TELEFAX:  404-815-6555
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2847 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  single
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;     HYPOTHETICAL:  NO
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;       ORGANISM:  Homo sapiens
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank HUMDAF; HUMDAFC1
;       CLONE:  Human DAF cDNA
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  1..819
;       OTHER INFORMATION:  /note= "HUMDAFC1 (Promotor and 5'
;       OTHER INFORMATION:  end of Exon 1, genomic sequence)"
PCT-US92-05920-2

  Query Match             59.7%;  Score 1255;  DB 5;  Length 2847;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1405;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db     811 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 870

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db     931 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 990

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Db    1051 TGACCTGCCTTAAGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 1110

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
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Db    1111 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 1170

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1171 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 1230

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1231 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 1290

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1291 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 1350

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1351 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 1410

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1411 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 1470

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1471 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 1530

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1531 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 1590

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1591 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 1650

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1651 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 1710

Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1711 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1770

Qy    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1771 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1830

Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1831 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1890

Qy    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1891 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1950

Qy    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1951 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 2010

Qy    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2011 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 2070

Qy    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2071 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 2130

Qy    1381 GTCCTGGAATCACATTCTTAGCACACCT 1408
           ||||||||||||||||||||||||||||
Db    2131 GTCCTGGAATCACATTCTTAGCACACCT 2158


RESULT 5
US-08-458-084-1
; Sequence 1, Application US/08458084
; Patent No. 5624837
;  GENERAL INFORMATION:
;    APPLICANT:  Fodor, William L
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Squinto, Stephen P
;    TITLE OF INVENTION:  Chimeric Complement
;    TITLE OF INVENTION:  Inhibitor Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
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;       SOFTWARE:  WordPerfect 6.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/458,084
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Klee, Maurice M.
;       REGISTRATION NUMBER:  30,399
;       REFERENCE/DOCKET NUMBER:  ALX-120
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (203) 255-1400
;       TELEFAX:  (203) 254-1101
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2096
;       TYPE:  Nucleic Acid
;       STRANDEDNESS:  Double
;       TOPOLOGY:  Linear
;     MOLECULE TYPE:  cDNA to mRNA
;     HYPOTHETICAL:  No
;     ANTI-SENSE:  No
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
;     PUBLICATION INFORMATION:
;       AUTHORS:  Lublin, Douglas M.
;       AUTHORS:  Atkinson, John P.
;       TITLE:  Decay-Accelerating Factor:
;       TITLE:  Biochemistry, Molecular Biology, and
;       TITLE:  Function
;       JOURNAL:  Annual Review of Immunology
;       VOLUME:  7
;       PAGES:  35-58
;       DATE:  1989
US-08-458-084-1

  Query Match             59.1%;  Score 1243;  DB 1;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
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Db    1381 CATTCTTAGCACACCT 1396


RESULT 6
US-08-205-508-1
; Sequence 1, Application US/08205508
; Patent No. 5627264
;  GENERAL INFORMATION:
;    APPLICANT:  Fodor, William L
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Squinto, Stephen P
;    TITLE OF INVENTION:  Chimeric Complement
;    TITLE OF INVENTION:  Inhibitor Proteins
```

```
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/205,508
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
US-08-205-508-1

  Query Match           59.1%;  Score 1243;  DB 1;  Length 2096;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
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Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
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Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
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Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
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Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
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Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
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Db    1381 CATTCTTAGCACACCT 1396
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RESULT 7
US-08-278-630A-10
; Sequence 10, Application US/08278630A
; Patent No. 5643770
;  GENERAL INFORMATION:
;    APPLICANT:  Mason, James M.
;    APPLICANT:  Squinto, Stephen P.
;    TITLE OF INVENTION:  Retroviral Vector Particles
;    TITLE OF INVENTION:  Expressing Complement Inhibitor Activity
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/278,630A
;      FILING DATE:  July 21, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-147
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
US-08-278-630A-10

  Query Match            59.1%;  Score 1243;  DB 1;  Length 2096;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
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Db   1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy   1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy   1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy   1393 CATTCTTAGCACACCT 1408
          ||||||||||||||||
Db   1381 CATTCTTAGCACACCT 1396


RESULT 8
PCT-US95-02945-1
; Sequence 1, Application PC/TUS9502945
;  GENERAL INFORMATION:
;    APPLICANT:  Fodor, William L
;    APPLICANT:  Rollins, Scott
;    APPLICANT:  Squinto, Stephen P
;    TITLE OF INVENTION:  Chimeric Complement
;    TITLE OF INVENTION:  Inhibitor Proteins
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Maurice M. Klee
;      STREET:  1951 Burr Street
;      CITY:  Fairfield
;      STATE:  Connecticut
;      COUNTRY:  USA
;      ZIP:  06430
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 750 Kb storage
;      COMPUTER:  Dell 486/50
;      OPERATING SYSTEM:  DOS 6.2
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/02945
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/205,508
;      FILING DATE:  3-MAR-1994
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Klee, Maurice M.
;      REGISTRATION NUMBER:  30,399
;      REFERENCE/DOCKET NUMBER:  ALX-120PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (203) 255-1400
;      TELEFAX:  (203) 254-1101
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2096
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Double
;      TOPOLOGY:  Linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  No
;    ANTI-SENSE:  No
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    PUBLICATION INFORMATION:
;      AUTHORS:  Lublin, Douglas M.
;      AUTHORS:  Atkinson, John P.
;      TITLE:  Decay-Accelerating Factor:
;      TITLE:  Biochemistry, Molecular Biology, and
;      TITLE:  Function
;      JOURNAL:  Annual Review of Immunology
;      VOLUME:  7
;      PAGES:  35-58
;      DATE:  1989
PCT-US95-02945-1

  Query Match           59.1%;  Score 1243;  DB 5;  Length 2096;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy     13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
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Db      1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy     73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy    133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy    193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy    253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy    433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
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Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy    913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy    973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
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Db    961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy   1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy   1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy   1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy   1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy   1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy   1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy   1393 CATTCTTAGCACACCT 1408
          ||||||||||||||||
Db   1381 CATTCTTAGCACACCT 1396


RESULT 9
US-07-811-048-10
; Sequence 10, Application US/07811048
; Patent No. 5264357
;  GENERAL INFORMATION:
;    APPLICANT:  Caras, Ingrid W.
;    TITLE OF INVENTION:  Nucleic Acid and Methods for the Synthesis of No. 5264357el Fu
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/811,048
;      FILING DATE:  19911219
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/738171
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  06/859107
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US86/01177
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/083757
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Benson, Robert H.
;      REGISTRATION NUMBER:  30,446
;      REFERENCE/DOCKET NUMBER:  330p1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/266-1489
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2234 bases
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-811-048-10

  Query Match             54.6%;  Score 1147;  DB 1;  Length 2234;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy    1141 TATCTGG 1147
           |||||||
Db    1141 TATCTGG 1147


RESULT 10
US-09-475-460A-31
; Sequence 31, Application US/09475460A
; Patent No. 6316253
; GENERAL INFORMATION:
;  APPLICANT:  Scott, Elizabeth
;  APPLICANT:  Innis, Michael
;  TITLE OF INVENTION:  EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE:  1527.003
;  CURRENT APPLICATION NUMBER: US/09/475,460A
;  CURRENT FILING DATE:  1999-12-30
;  NUMBER OF SEQ ID NOS:  32
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1848
;   TYPE: DNA
;   ORGANISM: CAB2
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1839)
US-09-475-460A-31

  Query Match            46.1%;  Score 970;  DB 4;  Length 1848;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  970;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     167 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 929

Qy     227 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 989

Qy     287 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 1049

Qy     347 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 1109

Qy     407 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 1169

Qy     467 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1170 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 1229

Qy     527 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 1289

Qy     587 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 646
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1290 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 1349

Qy     647 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 706
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1350 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 1409

Qy     707 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1410 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 1469

Qy     767 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1470 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 1529

Qy     827 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1530 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1589

Qy     887 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 946
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1590 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1649

Qy     947 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1006
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1650 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1709

Qy    1007 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1066
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1710 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1769

Qy    1067 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1770 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1829

Qy    1127 TACTACCCGT 1136
           ||||||||||
Db    1830 TACTACCCGT 1839


RESULT 11
US-09-748-061A-31
; Sequence 31, Application US/09748061A
; Patent No. 6451539
; GENERAL INFORMATION:
;  APPLICANT: Scott, Elizabeth
;  APPLICANT:  Innis, Michael
;  TITLE OF INVENTION: EXPRESSION VECTORS, TRANSFECTION SYSTEMS, AND METHOD OF
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: PP01527.101 / 2302-1527.10
;  CURRENT APPLICATION NUMBER: US/09/748,061A
;  CURRENT FILING DATE:  2000-12-22
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
;   LENGTH: 1848
;   TYPE: DNA
;   ORGANISM: CAB2
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7)..(1839)
US-09-748-061A-31

  Query Match            46.1%;  Score 970;  DB 4;  Length 1848;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches  970;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     167 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 929

Qy     227 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 286
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Db    930 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 989

Qy    287 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 1049

Qy    347 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 1109

Qy    407 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 1169

Qy    467 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 1229

Qy    527 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 1289

Qy    587 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 1349

Qy    647 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 1409

Qy    707 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 1469

Qy    767 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1470 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 1529

Qy    827 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1530 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1589

Qy    887 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1590 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1649

Qy    947 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1650 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1709

Qy   1007 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1710 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1769

Qy   1067 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1770 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1829

Qy   1127 TACTACCCGT 1136
          ||||||||||
Db   1830 TACTACCCGT 1839


RESULT 12
US-08-435-149-17
; Sequence 17, Application US/08435149
; Patent No. 5866402
;  GENERAL INFORMATION:
;    APPLICANT:  INNIS, MICHAEL A.
;    APPLICANT:  ZAROR, ISABEL
;    APPLICANT:  CREASEY, ABLA A.
;    TITLE OF INVENTION:  CHIMERIC MCP AND DAF PROTEINS WITH CELL
;    TITLE OF INVENTION:  SURFACE LOCALIZING DOMAIN
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION
;      STREET:  INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
;      CITY:  EMERYVILLE
;      STATE:  CALIFORNIA
;      COUNTRY:  U.S.A.
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/435,149
;      FILING DATE:  05-MAY-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAVEREIDE, PAUL B.
;      REGISTRATION NUMBER:  36,914
;      REFERENCE/DOCKET NUMBER:  0989.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2585
;      TELEFAX:  (510) 655-3542
;      TELEX:  N/A
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1878 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-435-149-17

  Query Match             46.1%;  Score 970;  DB 2;  Length 1878;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  970;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    167 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 226
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Db    906 TGACTGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAG 965

Qy    227 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 286
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 TTTTCCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGG 1025

Qy    287 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1026 CGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTG 1085

Qy    347 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1086 CAATCGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATAT 1145

Qy    407 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1146 CACTCAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAG 1205

Qy    467 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 526
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1206 AAGAGAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGC 1265

Qy    527 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1266 AGTCGAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGAT 1325

Qy    587 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1326 TGATGTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTA 1385

Qy    647 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 706
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Db   1386 CAAATTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAG 1445

Qy    707 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1446 TGACCCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGG 1505

Qy    767 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1506 AATAATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAA 1565

Qy    827 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1566 TAAAGGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGG 1625

Qy    887 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1626 AGAGTGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACC 1685

Qy    947 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1686 AACAGTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCA 1745

Qy   1007 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1746 GAAAACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTC 1805

Qy   1067 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1806 CAGGACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGG 1865

Qy   1127 TACTACCCGT 1136
          ||||||||||
Db   1866 TACTACCCGT 1875


RESULT 13
US-08-310-416A-12
; Sequence 12, Application US/08310416A
; Patent No. 5679546
;  GENERAL INFORMATION:
;    APPLICANT:  Jone-Long Ko et al.
;    TITLE OF INVENTION:  CHIMERIC PROTEINS WHICH BLOCK
;    TITLE OF INVENTION:  COMPLEMENT ACTIVATION
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,416A
;      FILING DATE:  22-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul T. Clark
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06180/005001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  969 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-310-416A-12

  Query Match             38.8%;  Score 816;  DB 1;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  816;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     561 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 620
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Db     574 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 633

Qy     801 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 860
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Db     634 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 693

Qy     861 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 920
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Qy     981 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 1040
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Db     934 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGT 969


RESULT 14
US-08-888-171-12
; Sequence 12, Application US/08888171
; Patent No. 5851528
;  GENERAL INFORMATION:
;    APPLICANT:  Jone-Long, Ko
;    APPLICANT:  Higgins, Paul J.
;    APPLICANT:  Yeh, C. Grace
```

```
;    TITLE OF INVENTION:  METHODS OF INHIBITING COMPLEMENT
;    TITLE OF INVENTION:  ACTIVATION
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/888,171
;      FILING DATE:  03-JUL-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/310,416
;      FILING DATE:  22-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06180/005002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/542-507
;      TELEFAX:  617/542-890
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  969 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-888-171-12

  Query Match             38.8%;  Score 816;  DB 2;  Length 969;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  816;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy     381 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 440
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Qy     441 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 500
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Qy     561 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 620
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Db     394 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 453

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Db     454 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 513

Qy     681 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     514 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 573

Qy     741 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 800
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Db     574 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 633

Qy     801 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 860
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Qy     861 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 920
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Qy     921 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 980
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Qy     981 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 1040
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Qy    1041 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1100
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RESULT 15
US-08-310-416A-19
; Sequence 19, Application US/08310416A
; Patent No. 5679546
;  GENERAL INFORMATION:
;    APPLICANT:  Jone-Long Ko et al.
;    TITLE OF INVENTION:  CHIMERIC PROTEINS WHICH BLOCK
;    TITLE OF INVENTION:  COMPLEMENT ACTIVATION
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  U.S.A.
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      COMPUTER:  IBM PS/2 Model 50Z or 55SX
;      OPERATING SYSTEM:  MS-DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/310,416A
;      FILING DATE:  22-SEP-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Paul T. Clark
;      REGISTRATION NUMBER:  30,162
;      REFERENCE/DOCKET NUMBER:  06180/005001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 542-5070
;      TELEFAX:  (617) 542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  860 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-310-416A-19

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  Matches  857;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Perfect score: 2102
Sequence: 1 ccgctgggcgtagctgcgac.....aaatgatcccatttttggt 2102

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2102 | 100.0 | 2102 | 20 | AAX87914 | Human CD55 tumour |
| 2 | 2102 | 100.0 | 2102 | 24 | ABK83991 | Human cDNA differe |
| 3 | 2102 | 100.0 | 2102 | 24 | ABL65229 | Lung cancer relate |
| 4 | 2102 | 100.0 | 2302 | 22 | AAH34999 | Human colon cancer |
| 5 | 1968 | 93.6 | 2263 | 22 | AAH23076 | Osteoarthritis tis |
| 6 | 1582 | 75.3 | 2115 | 16 | AAQ79863 | Decay accelerating |
| 7 | 1530 | 72.8 | 2115 | 10 | AAN91043 | Decay accelerating |
| 8 | 1401 | 66.7 | 2015 | 8 | AAN70047 | Encodes human deca |
| 9 | 1356 | 64.5 | 1493 | 20 | AAX87915 | Human tumour assoc |
| 10 | 1243 | 59.1 | 2096 | 16 | AAQ99105 | Human DAF cDNA. H |
| 11 | 1243 | 59.1 | 2096 | 18 | AAT84471 | Human DAF cDNA. H |
| 12 | 1147 | 54.6 | 2233 | 8 | AAN70048 | Encodes human deca |
| 13 | 1147 | 54.6 | 2233 | 10 | AAN91044 | Membrane bound dec |
| 14 | 1147 | 54.6 | 2233 | 16 | AAQ79864 | Decay accelerating |
| 15 | 1146 | 54.5 | 1146 | 20 | AAV08935 | DAF protein coding |
| 16 | 1097 | 52.2 | 2237 | 18 | AAT90287 | Human glycophospha |
| 17 | 1011 | 48.1 | 2416 | 22 | AAH57446 | Human lung cell sp |
| 18 | 970 | 46.1 | 1848 | 22 | AAD20355 | CAB2 protein encod |
| 19 | 970 | 46.1 | 1848 | 22 | AAD08170 | CAB-2 DNA. Uniden |
| 20 | 970 | 46.1 | 1848 | 24 | AAD27308 | CAB2 protein encod |
| 21 | 970 | 46.1 | 1878 | 17 | AAT46065 | Membrane co-factor |
| 22 | 957 | 45.5 | 1077 | 20 | AAZ77541 | Human ovarian tumo |
| c 23 | 279 | 13.3 | 586 | 24 | ABL67412 | Thyroid cancer rel |
| 24 | 277 | 13.2 | 1925 | 22 | AAH72967 | Human cervical can |
| 25 | 241 | 11.5 | 368 | 24 | ABL86715 | Human ovarian canc |
| c 26 | 240 | 11.4 | 479 | 23 | AAS58610 | cDNA #1286 encodin |
| 27 | 231 | 11.0 | 1104 | 15 | AAQ58894 | Sequence encoding |
| c 28 | 221 | 10.5 | 224 | 24 | ABL38333 | Human colon tumour |
| 29 | 196 | 9.3 | 548 | 21 | AAC98358 | Human colon cancer |
| 30 | 192 | 9.1 | 6565 | 22 | AAK91489 | Human digestive sy |
| 31 | 192 | 9.1 | 16141 | 22 | AAK73262 | Human immune/haema |
| 32 | 192 | 9.1 | 16141 | 22 | AAK91491 | Human digestive sy |
| 33 | 183 | 8.7 | 337 | 22 | AAL08160 | Human breast cance |
| 34 | 183 | 8.7 | 338 | 22 | AAL19070 | Human breast cance |
| 35 | 181 | 8.6 | 328 | 22 | AAL25905 | Human breast cance |
| 36 | 115 | 5.5 | 747 | 18 | AAT97175 | DR alpha-DAF chime |
| 37 | 114 | 5.4 | 134 | 18 | AAT97173 | Decay accelerating |
| 38 | 114 | 5.4 | 786 | 18 | AAT97176 | DR beta-1-DAF chim |
| 39 | 107 | 5.1 | 990 | 17 | AAT15927 | Neural cell adhesi |
| c 40 | 74 | 3.5 | 227 | 21 | AAC18250 | Human secreted pro |
| 41 | 71 | 3.4 | 418 | 20 | AAX30170 | Human secreted pro |
| c 42 | 61 | 2.9 | 61 | 22 | AAH57238 | Human lung specifi |
| 43 | 60 | 2.9 | 60 | 24 | ABN38712 | Human spliced tran |
| 44 | 52 | 2.5 | 3033 | 21 | AAZ29720 | Modified T. cruzi |
| c 45 | 44 | 2.1 | 44 | 16 | AAQ99120 | DAF oligo 176 -- 3 |
| 46 | 39 | 1.9 | 39 | 16 | AAQ99119 | DAF oligo 175 -- 5 |
| 47 | 34 | 1.6 | 35 | 22 | AAD20339 | PCR primer, DAFTH5 |
| 48 | 34 | 1.6 | 35 | 22 | AAD08154 | PCR primer CAB2H5- |
| 49 | 34 | 1.6 | 35 | 24 | AAD27292 | PCR primer, DAFTH5 |
| 50 | 34 | 1.6 | 39 | 24 | ABL52524 | Human DAF PCR prim |
| 51 | 32 | 1.5 | 1637 | 20 | AAZ30973 | Porcine complement |
| 52 | 31 | 1.5 | 40 | 16 | AAQ99121 | Oligo 173. Synthe |
| c 53 | 30 | 1.4 | 33 | 22 | AAD20338 | PCR primer, CAB2H3 |
| c 54 | 30 | 1.4 | 33 | 22 | AAD08153 | PCR primer CAB2H3- |
| c 55 | 30 | 1.4 | 33 | 24 | AAD27291 | PCR primer, CAB2H3 |
| c 56 | 29 | 1.4 | 34 | 16 | AAQ99122 | Oligo 174. Synthe |
| 57 | 26 | 1.2 | 33 | 16 | AAQ87502 | DAF-N2 PCR primer. |
| 58 | 25 | 1.2 | 39 | 16 | AAQ87497 | DAF-N5 PCR primer. |
| c 59 | 24 | 1.1 | 45 | 16 | AAQ87498 | DAF-C5 PCR primer. |
| c 60 | 24 | 1.1 | 106 | 22 | AAD20354 | PCR primer, CAB4-3 |
| c 61 | 24 | 1.1 | 106 | 22 | AAD08169 | Primer CAB4-33P fo |
| c 62 | 24 | 1.1 | 106 | 24 | AAD27307 | Primer, CAB4-33P t |
| 63 | 24 | 1.1 | 978 | 20 | AAZ30974 | Porcine complement |
| c 64 | 23 | 1.1 | 30 | 24 | ABL52525 | Human DAF PCR prim |
| c 65 | 23 | 1.1 | 39 | 22 | AAD20351 | PCR primer, DAFSXB |
| c 66 | 23 | 1.1 | 10690 | 23 | ABL05498 | Drosophila melanog |
| 67 | 22 | 1.0 | 22 | 19 | AAV54662 | Complement DAF mRN |
| c 68 | 22 | 1.0 | 22 | 19 | AAV54663 | Complement DAF mRN |
| 69 | 22 | 1.0 | 28 | 15 | AAQ58889 | Primer for amplify |
| c 70 | 22 | 1.0 | 31 | 16 | AAQ87503 | DAF-C2R PCR primer |
| c 71 | 22 | 1.0 | 33 | 15 | AAQ58883 | Primer for amplify |
| c 72 | 22 | 1.0 | 47 | 16 | AAQ99116 | cCIP DC oligo 55 - |
| c 73 | 22 | 1.0 | 2190 | 24 | AAS18067 | Ashbya gossypii AG |
| c 74 | 22 | 1.0 | 4510 | 23 | ABL20209 | Drosophila melanog |
| c 75 | 22 | 1.0 | 4785 | 23 | ABL13743 | Drosophila melanog |
| c 76 | 22 | 1.0 | 4852 | 23 | ABL09963 | Drosophila melanog |
| 77 | 22 | 1.0 | 6112 | 24 | ABL32662 | Human immune syste |
| c 78 | 22 | 1.0 | 6112 | 24 | ABL32663 | Human immune syste |
| c 79 | 22 | 1.0 | 7005 | 23 | ABL15355 | Drosophila melanog |
| c 80 | 22 | 1.0 | 13075 | 23 | ABL15354 | Drosophila melanog |
| 81 | 22 | 1.0 | 13631 | 23 | ABL20354 | Drosophila melanog |
| c 82 | 22 | 1.0 | 22788 | 23 | ABL20208 | Drosophila melanog |

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 83 | 22 | 1.0 | 44456 | 23 | ABL09962 |
| c | 84 | 22 | 1.0 | 49431 | 23 | ABL13742 |
| c | 85 | 21 | 1.0 | 21 | 20 | AAX87918 |
| | 86 | 21 | 1.0 | 198 | 22 | ABA47703 |
| | 87 | 21 | 1.0 | 198 | 22 | ABA65597 |
| | 88 | 21 | 1.0 | 198 | 22 | ABA32685 |
| | 89 | 21 | 1.0 | 198 | 22 | AAK14000 |
| | 90 | 21 | 1.0 | 198 | 22 | AAK39748 |
| | 91 | 21 | 1.0 | 198 | 22 | AAI20554 |
| | 92 | 21 | 1.0 | 198 | 22 | AAI45764 |
| | 93 | 21 | 1.0 | 198 | 22 | AAI06253 |
| | 94 | 21 | 1.0 | 198 | 24 | ABS13842 |
| | 95 | 21 | 1.0 | 428 | 22 | AAI82551 |
| | 96 | 21 | 1.0 | 448 | 22 | ABA42574 |
| | 97 | 21 | 1.0 | 448 | 22 | ABA53003 |
| | 98 | 21 | 1.0 | 448 | 22 | ABA22778 |
| | 99 | 21 | 1.0 | 448 | 22 | AAK01251 |
| | 100 | 21 | 1.0 | 448 | 22 | AAK26713 |
| | 101 | 21 | 1.0 | 448 | 22 | AAI11339 |
| | 102 | 21 | 1.0 | 448 | 22 | AAI32608 |
| | 103 | 21 | 1.0 | 448 | 22 | AAI01255 |
| | 104 | 21 | 1.0 | 448 | 24 | ABS01307 |
| | 105 | 21 | 1.0 | 465 | 17 | AAT13969 |
| | 106 | 21 | 1.0 | 465 | 20 | AAX89273 |
| | 107 | 21 | 1.0 | 466 | 17 | AAT13968 |
| | 108 | 21 | 1.0 | 466 | 20 | AAX89272 |
| | 109 | 21 | 1.0 | 682 | 24 | ABQ48408 |
| c | 110 | 21 | 1.0 | 682 | 24 | ABQ48409 |
| | 111 | 21 | 1.0 | 1776 | 21 | AAA71636 |
| | 112 | 21 | 1.0 | 2094 | 21 | AAA71623 |
| | 113 | 21 | 1.0 | 2143 | 22 | AAI60333 |
| | 114 | 21 | 1.0 | 2575 | 20 | AAZ10654 |
| | 115 | 21 | 1.0 | 2584 | 20 | AAZ10676 |
| | 116 | 21 | 1.0 | 2627 | 22 | AAI58547 |
| c | 117 | 21 | 1.0 | 4122 | 23 | ABL28439 |
| | 118 | 21 | 1.0 | 5829 | 24 | ABL33726 |
| | 119 | 21 | 1.0 | 6159 | 24 | ABN80236 |
| c | 120 | 21 | 1.0 | 6159 | 24 | ABN80237 |
| | 121 | 21 | 1.0 | 6301 | 24 | ABN80101 |
| | 122 | 21 | 1.0 | 6583 | 24 | ABL49325 |
| c | 123 | 21 | 1.0 | 6708 | 23 | ABL28438 |
| | 124 | 21 | 1.0 | 6782 | 24 | ABL32777 |
| | 125 | 21 | 1.0 | 9547 | 24 | ABL33504 |
| | 126 | 21 | 1.0 | 11684 | 22 | AAK66109 |
| c | 127 | 21 | 1.0 | 15923 | 23 | ABL07596 |
| | 128 | 21 | 1.0 | 32150 | 22 | AAS32454 |
| c | 129 | 21 | 1.0 | 74037 | 24 | ABK94412 |
| c | 130 | 21 | 1.0 | 168575 | 22 | AAH21613 |
| | 131 | 20 | 1.0 | 20 | 18 | AAT63597 |
| c | 132 | 20 | 1.0 | 20 | 18 | AAT63598 |
| c | 133 | 20 | 1.0 | 30 | 20 | AAX87920 |
| | 134 | 20 | 1.0 | 34 | 16 | AAQ99115 |
| c | 135 | 20 | 1.0 | 52 | 17 | AAT46068 |
| c | 136 | 20 | 1.0 | 55 | 17 | AAT46074 |
| c | 137 | 20 | 1.0 | 58 | 17 | AAT46073 |
| c | 138 | 20 | 1.0 | 73 | 17 | AAT46066 |
| c | 139 | 20 | 1.0 | 103 | 17 | AAT46069 |
| | 140 | 20 | 1.0 | 200 | 19 | AAV86016 |
| | 141 | 20 | 1.0 | 226 | 22 | AAH35354 |
| | 142 | 20 | 1.0 | 405 | 24 | ABN16614 |
| c | 143 | 20 | 1.0 | 1365 | 23 | ABL17751 |
| c | 144 | 20 | 1.0 | 1380 | 23 | ABL16541 |
| | 145 | 20 | 1.0 | 1561 | 19 | AAV27384 |
| | 146 | 20 | 1.0 | 1561 | 24 | ABQ84852 |
| | 147 | 20 | 1.0 | 1599 | 19 | AAV86017 |
| | 148 | 20 | 1.0 | 1711 | 19 | AAV86015 |
| c | 149 | 20 | 1.0 | 1836 | 17 | AAT33630 |
| c | 150 | 20 | 1.0 | 2008 | 22 | AAH15972 |
| | 151 | 20 | 1.0 | 2124 | 24 | ABL34260 |
| | 152 | 20 | 1.0 | 2132 | 24 | ABL50334 |
| | 153 | 20 | 1.0 | 2194 | 22 | AAF93912 |
| c | 154 | 20 | 1.0 | 2402 | 23 | ABL03061 |
| | 155 | 20 | 1.0 | 2558 | 24 | AAD28948 |

| |
|---|
| Drosophila melanog |
| Drosophila melanog |
| Human tumour assoc |
| Human breast cell |
| Human foetal liver |
| Probe #11151 for g |
| Human brain expres |
| Human bone marrow |
| Probe #10487 for g |
| Probe #14450 used |
| Probe #6244 used t |
| Human genome-deriv |
| Human polynucleoti |
| Human breast cell |
| Human foetal liver |
| Probe #1244 for ge |
| Human brain expres |
| Human bone marrow |
| Probe #1272 for ge |
| Probe #1294 used t |
| Probe #1246 used t |
| Human genome-deriv |
| Eimeria gametocyte |
| Partial DNA sequen |
| Eimeria gametocyte |
| Partial DNA sequen |
| Oligonucleotide fo |
| Oligonucleotide fo |
| Human aspartate pr |
| Human aspartate pr |
| Human polynucleoti |
| cDNA encoding a hu |
| cDNA encoding a hu |
| Human polynucleoti |
| Drosophila melanog |
| Human immune syste |
| Human chemically m |
| Human chemically m |
| Human chemically m |
| Human polynucleoti |
| Drosophila melanog |
| Human immune syste |
| Human immune syste |
| Human immune/haema |
| Drosophila melanog |
| Human genomic DNA |
| DNA encoding endot |
| Human hypocretin r |
| CD55 PCR primer us |
| CD55 PCR primer us |
| Human tumour assoc |
| cCIP DC oligo 54 - |
| Heparin binding pe |
| Fibronectin hepari |
| Fibronectin hepari |
| Heparin binding pe |
| TFPI heparin bindi |
| 5'-extension of th |
| Human colon cancer |
| Human ORFX polynuc |
| Drosophila melanog |
| Drosophila melanog |
| Streptococcus pneu |
| S. pneumoniae SP07 |
| Mouse Lrp5 cDNA op |
| Mouse Lrp5 cDNA po |
| Rat p65 oncofoetal |
| Human cDNA sequenc |
| Human immune syste |
| Human cancer cell |
| Human cDNA encodin |
| Drosophila melanog |
| Human MOL5b cDNA. |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 156 | 20 | 1.0 | 2621 | 23 | ABL21976 |
| | 157 | 20 | 1.0 | 2811 | 22 | AAF29451 |
| | 158 | 20 | 1.0 | 2813 | 24 | ABN59626 |
| c | 159 | 20 | 1.0 | 2995 | 23 | ABL26580 |
| | 160 | 20 | 1.0 | 3104 | 23 | ABL13938 |
| | 161 | 20 | 1.0 | 3112 | 24 | AAD28949 |
| | 162 | 20 | 1.0 | 3121 | 19 | AAV27382 |
| | 163 | 20 | 1.0 | 3121 | 24 | ABQ84850 |
| | 164 | 20 | 1.0 | 3293 | 22 | AAD08048 |
| c | 165 | 20 | 1.0 | 3365 | 23 | ABL17750 |
| | 166 | 20 | 1.0 | 3776 | 24 | ABN83983 |
| | 167 | 20 | 1.0 | 3868 | 24 | AAD28947 |
| c | 168 | 20 | 1.0 | 4099 | 23 | ABL28045 |
| | 169 | 20 | 1.0 | 4843 | 19 | AAV70399 |
| | 170 | 20 | 1.0 | 5117 | 19 | AAV86018 |
| | 171 | 20 | 1.0 | 5119 | 24 | ABA94317 |
| c | 172 | 20 | 1.0 | 5690 | 22 | AAK81236 |
| c | 173 | 20 | 1.0 | 5690 | 22 | AAK81239 |
| | 174 | 20 | 1.0 | 5829 | 24 | ABK67855 |
| c | 175 | 20 | 1.0 | 7213 | 23 | ABL11466 |
| c | 176 | 20 | 1.0 | 7326 | 16 | AAQ99456 |
| c | 177 | 20 | 1.0 | 7326 | 19 | AAV10093 |
| c | 178 | 20 | 1.0 | 7326 | 21 | AAA62948 |
| c | 179 | 20 | 1.0 | 7326 | 21 | AAA15554 |
| | 180 | 20 | 1.0 | 7607 | 24 | ABL34615 |
| | 181 | 20 | 1.0 | 7980 | 19 | AAV44243 |
| c | 182 | 20 | 1.0 | 8381 | 23 | ABL07398 |
| c | 183 | 20 | 1.0 | 10170 | 23 | ABL16540 |
| | 184 | 20 | 1.0 | 10467 | 24 | ABL49302 |
| c | 185 | 20 | 1.0 | 14409 | 23 | ABL26290 |
| | 186 | 20 | 1.0 | 14736 | 19 | AAV52304 |
| | 187 | 20 | 1.0 | 14771 | 23 | ABL28044 |
| | 188 | 20 | 1.0 | 18434 | 24 | ABL34006 |
| | 189 | 20 | 1.0 | 30942 | 23 | ABL07216 |
| c | 190 | 20 | 1.0 | 36383 | 23 | ABL05364 |
| | 191 | 20 | 1.0 | 53552 | 22 | AAS13655 |
| | 192 | 20 | 1.0 | 57248 | 24 | ABK83563 |
| c | 193 | 20 | 1.0 | 130263 | 24 | ABK83573 |
| | 194 | 20 | 1.0 | 227968 | 24 | ABK83497 |
| | 195 | 19 | 0.9 | 19 | 20 | AAX87916 |
| c | 196 | 19 | 0.9 | 19 | 20 | AAX87921 |
| | 197 | 19 | 0.9 | 19 | 20 | AAX87922 |
| c | 198 | 19 | 0.9 | 33 | 22 | AAD20353' |
| c | 199 | 19 | 0.9 | 33 | 22 | AAD08168 |
| c | 200 | 19 | 0.9 | 33 | 24 | AAD27306 |
| | 201 | 19 | 0.9 | 89 | 19 | AAV68382 |
| | 202 | 19 | 0.9 | 182 | 21 | AAA45195 |
| c | 203 | 19 | 0.9 | 279 | 24 | ABN20365 |
| c | 204 | 19 | 0.9 | 290 | 23 | ABL28709 |
| c | 205 | 19 | 0.9 | 303 | 23 | ABL22389 |
| | 206 | 19 | 0.9 | 326 | 22 | AAK61755 |
| c | 207 | 19 | 0.9 | 326 | 23 | ABV47258 |
| | 208 | 19 | 0.9 | 329 | 21 | AAF20113 |
| | 209 | 19 | 0.9 | 329 | 21 | AAA33991 |
| c | 210 | 19 | 0.9 | 377 | 22 | AAI80435 |
| c | 211 | 19 | 0.9 | 525 | 23 | ABL22337 |
| c | 212 | 19 | 0.9 | 546 | 22 | AAF83929 |
| | 213 | 19 | 0.9 | 565 | 23 | ABV51648 |
| | 214 | 19 | 0.9 | 566 | 24 | ABQ33704 |
| c | 215 | 19 | 0.9 | 566 | 24 | ABQ33705 |
| | 216 | 19 | 0.9 | 672 | 22 | AAS21867 |
| | 217 | 19 | 0.9 | 714 | 24 | ABL56227 |
| | 218 | 19 | 0.9 | 738 | 21 | AAC48775 |
| c | 219 | 19 | 0.9 | 778 | 22 | AAI86678 |
| c | 220 | 19 | 0.9 | 804 | 23 | ABL26921 |
| | 221 | 19 | 0.9 | 828 | 15 | AAQ65357 |
| | 222 | 19 | 0.9 | 830 | 21 | AAC47864 |
| | 223 | 19 | 0.9 | 831 | 15 | AAQ65355 |
| | 224 | 19 | 0.9 | 967 | 24 | ABL39795 |
| c | 225 | 19 | 0.9 | 971 | 21 | AAA76283 |
| | 226 | 19 | 0.9 | 975 | 11 | AAQ04494 |
| c | 227 | 19 | 0.9 | 990 | 23 | ABL05665 |
| | 228 | 19 | 0.9 | 1037 | 21 | AAA88860 |

| |
|---|
| Drosophila melanog |
| Human TANGO 276 cD |
| Novel human coding |
| Drosophila melanog |
| Drosophila melanog |
| Human MOL5c cDNA. |
| Streptococcus pneu |
| S. pneumoniae SP07 |
| Human extracellula |
| Drosophila melanog |
| Human gene sequenc |
| Human MOL5a cDNA. |
| Drosophila melanog |
| Mouse Lrp5 cDNA. |
| Mouse Lrp5 full le |
| LPR5 polypeptide e |
| Human immune/haema |
| Human immune/haema |
| Lettuce pest resis |
| Drosophila melanog |
| Sequence encoding |
| Cellular transcrip |
| CREB binding prote |
| Mouse nuclear CREB |
| Human metastasis a |
| Lettuce resistance |
| Drosophila melanog |
| Drosophila melanog |
| Human polynucleoti |
| Drosophila melanog |
| Streptococcus pneu |
| Drosophila melanog |
| Human immune syste |
| Drosophila melanog |
| Drosophila melanog |
| Genomic DNA sequen |
| Human cDNA differe |
| Human cDNA differe |
| Human cDNA differe |
| Human tumour assoc |
| Human tumour assoc |
| Human tumour assoc |
| PCR primer, STTDEL |
| Primer STDELE31 fo |
| Primer, STDELE31 t |
| Clone #8 fragment |
| Human secreted exp |
| Human ORFX polynuc |
| Drosophila melanog |
| Drosophila melanog |
| Human immune/haema |
| Human prostate exp |
| Human adenosine A2 |
| Low adenosine anti |
| Human polynucleoti |
| Drosophila melanog |
| BAP28 genomic ampl |
| Human prostate exp |
| Oligonucleotide fo |
| Oligonucleotide fo |
| Human collagen gen |
| AmEPV forth RNA po |
| Arabidopsis thalia |
| Human polynucleoti |
| Drosophila melanog |
| Mouse brain natriu |
| Arabidopsis thalia |
| Mouse brain natriu |
| Human NS cDNA sequ |
| Maize glutathione- |
| Sequence encoding |
| Drosophila melanog |
| Human bone sialopr |

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 229 | 19 | 0.9 | 1043 | 21 | AAC55914 | Eucalyptus grandis |
| c | 230 | 19 | 0.9 | 1161 | 23 | ABL27627 | Drosophila melanog |
| c | 231 | 19 | 0.9 | 1239 | 21 | AAZ51240 | Staphylococcus aur |
| | 232 | 19 | 0.9 | 1281 | 24 | AAS17591 | DNA encoding novel |
| | 233 | 19 | 0.9 | 1282 | 23 | AAS87535 | DNA encoding novel |
| | 234 | 19 | 0.9 | 1287 | 21 | AAC76396 | Human ORFX ORF1951 |
| | 235 | 19 | 0.9 | 1352 | 24 | ABK14473 | Human protein phos |
| c | 236 | 19 | 0.9 | 1353 | 23 | ABL28449 | Drosophila melanog |
| | 237 | 19 | 0.9 | 1465 | 15 | AAQ65358 | Mouse brain natriu |
| | 238 | 19 | 0.9 | 1468 | 15 | AAQ65356 | Mouse brain natriu |
| c | 239 | 19 | 0.9 | 1560 | 23 | AAS86362 | DNA encoding novel |
| | 240 | 19 | 0.9 | 1566 | 24 | ABN66955 | Streptococcus poly |
| c | 241 | 19 | 0.9 | 1593 | 23 | AAS84243 | DNA encoding novel |
| c | 242 | 19 | 0.9 | 1713 | 23 | ABL18459 | Drosophila melanog |
| | 243 | 19 | 0.9 | 1827 | 22 | AAI99281 | Human excretory re |
| | 244 | 19 | 0.9 | 1827 | 22 | AAK78601 | Human immune/haema |
| | 245 | 19 | 0.9 | 1827 | 22 | AAI63631 | Human kidney relat |
| c | 246 | 19 | 0.9 | 2142 | 23 | ABL28147 | Drosophila melanog |
| | 247 | 19 | 0.9 | 2205 | 22 | AAS03912 | Human secreted pro |
| c | 248 | 19 | 0.9 | 2205 | 23 | ABL30123 | Drosophila melanog |
| c | 249 | 19 | 0.9 | 2205 | 23 | ABL04493 | Drosophila melanog |
| | 250 | 19 | 0.9 | 2205 | 23 | AAS86363 | DNA encoding novel |
| c | 251 | 19 | 0.9 | 2258 | 23 | ABL09468 | Drosophila melanog |
| | 252 | 19 | 0.9 | 2259 | 11 | AAQ05106 | Sequence encoding |
| | 253 | 19 | 0.9 | 2259 | 24 | ABN95609 | Gene #2107 used to |
| | 254 | 19 | 0.9 | 2259 | 24 | ABL62094 | Colon adenocarcino |
| | 255 | 19 | 0.9 | 2259 | 24 | ABL67543 | Thyroid cancer rel |
| | 256 | 19 | 0.9 | 2259 | 24 | ABL67945 | Ovary cancer relat |
| | 257 | 19 | 0.9 | 2259 | 24 | ABL68607 | Kidney cancer rela |
| c | 258 | 19 | 0.9 | 2267 | 18 | AAX63355 | Granule bound star |
| | 259 | 19 | 0.9 | 2290 | 23 | ABL28708 | Drosophila melanog |
| c | 260 | 19 | 0.9 | 2303 | 23 | ABL22388 | Drosophila melanog |
| | 261 | 19 | 0.9 | 2389 | 22 | AAF97924 | Human secreted pro |
| | 262 | 19 | 0.9 | 2398 | 24 | ABQ54557 | Human ovarian anti |
| | 263 | 19 | 0.9 | 2525 | 23 | ABL22336 | Drosophila melanog |
| c | 264 | 19 | 0.9 | 2572 | 23 | ABL23469 | Drosophila melanog |
| | 265 | 19 | 0.9 | 2619 | 24 | ABL56222 | AmEPV mRNA capping |
| c | 266 | 19 | 0.9 | 2738 | 23 | ABL08506 | Drosophila melanog |
| | 267 | 19 | 0.9 | 2744 | 16 | AAQ98470 | MiSP1-containing p |
| | 268 | 19 | 0.9 | 2745 | 22 | AAD09568 | Human transporter |
| | 269 | 19 | 0.9 | 2756 | 23 | ABL16958 | Drosophila melanog |
| | 270 | 19 | 0.9 | 2778 | 23 | ABL18614 | Drosophila melanog |
| | 271 | 19 | 0.9 | 2815 | 23 | ABV22085 | Human prostate exp |
| | 272 | 19 | 0.9 | 2815 | 23 | ABV27925 | Human prostate exp |
| c | 273 | 19 | 0.9 | 2831 | 23 | ABL09745 | Drosophila melanog |
| c | 274 | 19 | 0.9 | 2848 | 18 | AAT84155 | DNA encoding one u |
| c | 275 | 19 | 0.9 | 2848 | 19 | AAV53497 | DNA encoding a exo |
| | 276 | 19 | 0.9 | 2872 | 22 | AAK94922 | Human full-length |
| | 277 | 19 | 0.9 | 2911 | 24 | ABK47335 | cDNA encoding huma |
| | 278 | 19 | 0.9 | 2919 | 24 | AAD22780 | Human sulphate tra |
| | 279 | 19 | 0.9 | 2955 | 24 | AAD22782 | Human sulphate tra |
| | 280 | 19 | 0.9 | 3018 | 24 | ABK83911 | Human cDNA differe |
| | 281 | 19 | 0.9 | 3034 | 17 | AAT08715 | Calcitonin gene-re |
| | 282 | 19 | 0.9 | 3035 | 17 | AAT16876 | cDNA encoding a hu |
| c | 283 | 19 | 0.9 | 3069 | 14 | AAQ51015 | Rat opioid recepto |
| c | 284 | 19 | 0.9 | 3104 | 23 | ABL04869 | Drosophila melanog |
| | 285 | 19 | 0.9 | 3182 | 23 | ABL05664 | Drosophila melanog |
| c | 286 | 19 | 0.9 | 3190 | 23 | ABL07421 | Drosophila melanog |
| | 287 | 19 | 0.9 | 3221 | 23 | ABL26920 | Drosophila melanog |
| c | 288 | 19 | 0.9 | 3237 | 23 | ABL03607 | Drosophila melanog |
| | 289 | 19 | 0.9 | 3243 | 23 | ABL27626 | Drosophila melanog |
| c | 290 | 19 | 0.9 | 3489 | 23 | ABL28043 | Drosophila melanog |
| c | 291 | 19 | 0.9 | 3597 | 23 | ABL28448 | Drosophila melanog |
| c | 292 | 19 | 0.9 | 3769 | 23 | ABL12488 | Drosophila melanog |
| c | 293 | 19 | 0.9 | 3862 | 23 | ABL03155 | Drosophila melanog |
| c | 294 | 19 | 0.9 | 3903 | 23 | ABL22517 | Drosophila melanog |
| c | 295 | 19 | 0.9 | 3971 | 23 | ABL17923 | Drosophila melanog |
| c | 296 | 19 | 0.9 | 4151 | 23 | ABL17488 | Drosophila melanog |
| c | 297 | 19 | 0.9 | 4233 | 23 | ABL25099 | Drosophila melanog |
| c | 298 | 19 | 0.9 | 4252 | 23 | ABL13906 | Drosophila melanog |
| c | 299 | 19 | 0.9 | 4413 | 23 | ABL04492 | Drosophila melanog |
| c | 300 | 19 | 0.9 | 4628 | 23 | ABL23468 | Drosophila melanog |
| | 301 | 19 | 0.9 | 4896 | 23 | ABL28146 | Drosophila melanog |
| c | 302 | 19 | 0.9 | 4946 | 23 | ABL20728 | Drosophila melanog |
| | 303 | 19 | 0.9 | 5157 | 23 | ABL18458 | Drosophila melanog |
| | 304 | 19 | 0.9 | 5179 | 24 | ABL33996 | Human immune syste |
| | 305 | 19 | 0.9 | 5179 | 24 | ABK28403 | DNA transcription |
| | 306 | 19 | 0.9 | 5227 | 22 | AAK51712 | Human polynucleoti |
| c | 307 | 19 | 0.9 | 5352 | 22 | AAS04049 | Human ABC1 gene, p |
| c | 308 | 19 | 0.9 | 5567 | 23 | ABL07420 | Drosophila melanog |
| | 309 | 19 | 0.9 | 5674 | 23 | ABL26242 | Drosophila melanog |
| | 310 | 19 | 0.9 | 5747 | 24 | ABL52215 | Human phosphorylas |
| | 311 | 19 | 0.9 | 5747 | 24 | ABL52275 | Human phosphorylas |
| c | 312 | 19 | 0.9 | 5951 | 22 | AAS45409 | Chemically pretrea |
| c | 313 | 19 | 0.9 | 5951 | 24 | ABK28260 | DNA transcription |
| | 314 | 19 | 0.9 | 6034 | 23 | ABL22516 | Drosophila melanog |
| | 315 | 19 | 0.9 | 6052 | 24 | ABL32417 | Human immune syste |
| c | 316 | 19 | 0.9 | 6062 | 24 | AAS61094 | Human gene regulat |
| | 317 | 19 | 0.9 | 6081 | 24 | ABN80192 | Human chemically m |
| | 318 | 19 | 0.9 | 6081 | 24 | ABL33428 | Human immune syste |
| | 319 | 19 | 0.9 | 6175 | 24 | ABL33307 | Human immune syste |
| | 320 | 19 | 0.9 | 6189 | 22 | AAS46599 | Tumour suppressor |
| | 321 | 19 | 0.9 | 6189 | 24 | ABL34592 | Human metastasis a |
| | 322 | 19 | 0.9 | 6271 | 22 | AAS46455 | Tumour suppressor |
| | 323 | 19 | 0.9 | 6271 | 24 | ABK33977 | Human DNA for stag |
| | 324 | 19 | 0.9 | 6271 | 24 | ABL33336 | Human immune syste |
| | 325 | 19 | 0.9 | 6324 | 24 | ABK31542 | Signal transductio |
| c | 326 | 19 | 0.9 | 6406 | 23 | ABL09744 | Drosophila melanog |
| | 327 | 19 | 0.9 | 6412 | 24 | ABN80052 | Human chemically m |
| | 328 | 19 | 0.9 | 6412 | 24 | ABL70535 | Chemically treated |
| | 329 | 19 | 0.9 | 6412 | 24 | AAS61145 | Human gene regulat |
| | 330 | 19 | 0.9 | 6412 | 24 | ABK31232 | Signal transductio |
| | 331 | 19 | 0.9 | 6535 | 24 | ABL32936 | Human immune syste |
| c | 332 | 19 | 0.9 | 6722 | 24 | ABL32380 | Human immune syste |
| c | 333 | 19 | 0.9 | 6765 | 23 | ABL12336 | Drosophila melanog |
| | 334 | 19 | 0.9 | 6815 | 22 | AAS45344 | Chemically pretrea |
| | 335 | 19 | 0.9 | 6815 | 24 | ABL32670 | Human immune syste |
| | 336 | 19 | 0.9 | 6815 | 24 | ABK28175 | DNA transcription |
| | 337 | 19 | 0.9 | 6912 | 24 | ABK28371 | DNA transcription |
| c | 338 | 19 | 0.9 | 6923 | 24 | ABL70275 | Chemically treated |
| | 339 | 19 | 0.9 | 6923 | 24 | ABL70276 | Chemically treated |
| c | 340 | 19 | 0.9 | 6923 | 24 | AAS61198 | Human gene regulat |
| | 341 | 19 | 0.9 | 6923 | 24 | AAS61199 | Human gene regulat |
| c | 342 | 19 | 0.9 | 6923 | 24 | ABK31296 | Signal transductio |
| | 343 | 19 | 0.9 | 6923 | 24 | ABK31297 | Signal transductio |
| | 344 | 19 | 0.9 | 7001 | 24 | ABK33919 | Human DNA for stag |
| | 345 | 19 | 0.9 | 7028 | 23 | ABL30122 | Drosophila melanog |
| | 346 | 19 | 0.9 | 7080 | 23 | ABL10068 | Drosophila melanog |
| c | 347 | 19 | 0.9 | 7179 | 23 | ABL25098 | Drosophila melanog |
| c | 348 | 19 | 0.9 | 7234 | 24 | ABK31229 | Signal transductio |
| c | 349 | 19 | 0.9 | 7297 | 22 | ABA17018 | Human nervous syst |
| c | 350 | 19 | 0.9 | 7297 | 22 | ABA21221 | Human nervous syst |
| c | 351 | 19 | 0.9 | 7440 | 24 | ABL32425 | Human immune syste |
| | 352 | 19 | 0.9 | 7800 | 21 | AAF20842 | Human multiple tar |
| | 353 | 19 | 0.9 | 7800 | 21 | AAA34720 | Human adenosine re |
| | 354 | 19 | 0.9 | 7803 | 20 | AAX55272 | Human receptor-rel |
| | 355 | 19 | 0.9 | 7895 | 24 | ABK28364 | DNA transcription |
| c | 356 | 19 | 0.9 | 8673 | 23 | ABL11109 | Drosophila melanog |
| | 357 | 19 | 0.9 | 8842 | 24 | ABL33448 | Human immune syste |
| | 358 | 19 | 0.9 | 8842 | 24 | AAS63334 | Chemically pretrea |
| c | 359 | 19 | 0.9 | 9176 | 23 | ABL23200 | Drosophila melanog |
| c | 360 | 19 | 0.9 | 9326 | 21 | AAZ51236 | Staphylococcus aur |
| c | 361 | 19 | 0.9 | 9614 | 23 | ABL03154 | Drosophila melanog |
| | 362 | 19 | 0.9 | 9652 | 24 | ABL32909 | Human immune syste |
| c | 363 | 19 | 0.9 | 9797 | 20 | AAX13487 | Enterococcus faeca |
| c | 364 | 19 | 0.9 | 10280 | 22 | AAK68375 | Human immune/haema |
| | 365 | 19 | 0.9 | 11200 | 23 | ABL11108 | Drosophila melanog |
| | 366 | 19 | 0.9 | 12138 | 24 | ABK40033 | Human chemically p |
| | 367 | 19 | 0.9 | 12138 | 24 | ABL33628 | Human immune syste |
| c | 368 | 19 | 0.9 | 12465 | 22 | AAS45327 | Chemically pretrea |
| c | 369 | 19 | 0.9 | 12465 | 24 | ABL32635 | Human immune syste |
| c | 370 | 19 | 0.9 | 13321 | 22 | AAS46421 | Tumour suppressor |
| c | 371 | 19 | 0.9 | 15282 | 24 | ABL70190 | Chemically treated |
| c | 372 | 19 | 0.9 | 15282 | 24 | AAS61140 | Human gene regulat |
| | 373 | 19 | 0.9 | 16373 | 24 | ABL32618 | Human immune syste |
| | 374 | 19 | 0.9 | 16373 | 24 | ABL32619 | Human immune syste |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 375 | 19 | 0.9 | 16373 | 24 | AAD28382 |
| | 376 | 19 | 0.9 | 16373 | 24 | AAD28383 |
| c | 377 | 19 | 0.9 | 16560 | 23 | ABL17922 |
| | 378 | 19 | 0.9 | 17293 | 24 | ABL70125 |
| | 379 | 19 | 0.9 | 17293 | 24 | AAS61057 |
| | 380 | 19 | 0.9 | 17293 | 24 | ABK31170 |
| | 381 | 19 | 0.9 | 17310 | 18 | AAV74334 |
| | 382 | 19 | 0.9 | 17841 | 23 | ABL04868 |
| c | 383 | 19 | 0.9 | 19165 | 23 | ABL17898 |
| c | 384 | 19 | 0.9 | 19674 | 23 | ABL28042 |
| | 385 | 19 | 0.9 | 20892 | 22 | ABA15709 |
| | 386 | 19 | 0.9 | 21387 | 22 | AAS42161 |
| c | 387 | 19 | 0.9 | 22345 | 23 | ABL02352 |
| | 388 | 19 | 0.9 | 25576 | 22 | AAK69089 |
| | 389 | 19 | 0.9 | 26928 | 20 | AAZ32184 |
| | 390 | 19 | 0.9 | 26928 | 24 | ABN95780 |
| | 391 | 19 | 0.9 | 28660 | 23 | ABL03606 |
| | 392 | 19 | 0.9 | 31766 | 24 | AAD22781 |
| | 393 | 19 | 0.9 | 38682 | 22 | AAS21770 |
| c | 394 | 19 | 0.9 | 50000 | 24 | ABL56201 |
| | 395 | 19 | 0.9 | 114955 | 20 | AAX53491 |
| | 396 | 19 | 0.9 | 117609 | 21 | AAF21435 |
| | 397 | 19 | 0.9 | 123219 | 23 | AAH88703 |
| | 398 | 19 | 0.9 | 325791 | 22 | AAS43104 |
| | 399 | 18 | 0.9 | 21 | 20 | AAX87917 |
| | 400 | 18 | 0.9 | 25 | 18 | AAT76055 |
| | 401 | 18 | 0.9 | 25 | 20 | AAX53847 |
| | 402 | 18 | 0.9 | 25 | 21 | AAF19412 |
| | 403 | 18 | 0.9 | 25 | 21 | AAA33290 |
| | 404 | 18 | 0.9 | 25 | 21 | AAA03692 |
| | 405 | 18 | 0.9 | 29 | 20 | AAX87919 |
| | 406 | 18 | 0.9 | 30 | 17 | AAT46070 |
| c | 407 | 18 | 0.9 | 31 | 22 | AAD20352 |
| c | 408 | 18 | 0.9 | 31 | 22 | AAD08167 |
| c | 409 | 18 | 0.9 | 31 | 24 | AAD27305 |
| | 410 | 18 | 0.9 | 33 | 16 | AAQ99113 |
| c | 411 | 18 | 0.9 | 33 | 23 | ABI97602 |
| | 412 | 18 | 0.9 | 40 | 21 | AAZ49144 |
| c | 413 | 18 | 0.9 | 40 | 21 | AAZ49146 |
| | 414 | 18 | 0.9 | 40 | 21 | AAZ49156 |
| | 415 | 18 | 0.9 | 188 | 15 | AAQ71163 |
| | 416 | 18 | 0.9 | 202 | 22 | ABA74416 |
| | 417 | 18 | 0.9 | 202 | 22 | ABA39299 |
| | 418 | 18 | 0.9 | 202 | 22 | AAK22878 |
| | 419 | 18 | 0.9 | 202 | 22 | AAK49051 |
| | 420 | 18 | 0.9 | 202 | 22 | AAI26420 |
| | 421 | 18 | 0.9 | 202 | 22 | AAI54878 |
| | 422 | 18 | 0.9 | 202 | 24 | ABS22667 |
| c | 423 | 18 | 0.9 | 225 | 22 | AAD06217 |
| c | 424 | 18 | 0.9 | 225 | 23 | AAS55623 |
| | 425 | 18 | 0.9 | 255 | 22 | AAK57804 |
| c | 426 | 18 | 0.9 | 270 | 23 | ABV34504 |
| c | 427 | 18 | 0.9 | 270 | 23 | ABV43362 |
| c | 428 | 18 | 0.9 | 276 | 24 | ABN76916 |
| | 429 | 18 | 0.9 | 321 | 24 | ABN23319 |
| c | 430 | 18 | 0.9 | 335 | 22 | AAI98662 |
| c | 431 | 18 | 0.9 | 335 | 22 | AAI63058 |
| c | 432 | 18 | 0.9 | 409 | 24 | ABN79281 |
| c | 433 | 18 | 0.9 | 445 | 23 | ABV13386 |
| c | 434 | 18 | 0.9 | 448 | 24 | ABN73309 |
| c | 435 | 18 | 0.9 | 448 | 24 | ABN73399 |
| | 436 | 18 | 0.9 | 474 | 23 | ABV54699 |
| | 437 | 18 | 0.9 | 484 | 17 | AAT13967 |
| | 438 | 18 | 0.9 | 484 | 20 | AAX89271 |
| c | 439 | 18 | 0.9 | 500 | 21 | AAC94145 |
| | 440 | 18 | 0.9 | 501 | 24 | ABQ24888 |
| c | 441 | 18 | 0.9 | 501 | 24 | ABQ24889 |
| | 442 | 18 | 0.9 | 515 | 24 | ABQ51870 |
| c | 443 | 18 | 0.9 | 515 | 24 | ABQ51871 |
| | 444 | 18 | 0.9 | 527 | 21 | ABN81145 |
| | 445 | 18 | 0.9 | 527 | 23 | ABV53922 |
| | 446 | 18 | 0.9 | 533 | 21 | AAC54312 |
| c | 447 | 18 | 0.9 | 543 | 23 | ABL24689 |

| |
|---|
| Human chemically t |
| Human chemically t |
| Drosophila melanog |
| Chemically treated |
| Human gene regulat |
| Signal transductio |
| Staphylococcus aur |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Human nervous syst |
| Genomic sequence # |
| Drosophila melanog |
| Human immune/haema |
| Human prothrombin |
| Gene #2278 used to |
| Drosophila melanog |
| Human sulphate tra |
| Human gene for col |
| AmEPV genome fragm |
| Human adenosine A1 |
| Human receptor-rel |
| Human DNA sequence |
| Human Oestrogen re |
| Human tumour assoc |
| Human A2a adenosin |
| Human adenosine A2 |
| Human adenosine A2 |
| Low adenosine anti |
| Human adenosine A1 |
| Human tumour assoc |
| TFPI heparin bindi |
| PCR primer, STTDEL |
| Primer STTDELE3 fo |
| Primer, STTDELE3 t |
| cCIP DC oligo A -- |
| Endogenous human G |
| Probe for detectio |
| Probe for detectio |
| Probe for detectio |
| Merlin gene fragme |
| Human foetal liver |
| Probe #17765 for g |
| Human brain expres |
| Human bone marrow |
| Probe #16353 for g |
| Probe #23564 used |
| Human genome-deriv |
| Streptococcus pneu |
| Streptococcus pneu |
| Human immune/haema |
| Human prostate exp |
| Human prostate exp |
| Human ORF1863 cDNA |
| Human ORFX polynuc |
| Human excretory re |
| Human kidney relat |
| Human ORF4228 cDNA |
| Human prostate exp |
| Bovine embryonic g |
| Bovine embryonic g |
| Human prostate exp |
| Eimeria gametocyte |
| DNA sequence of cl |
| Cat flea head and |
| Oligonucleotide fo |
| Oligonucleotide fo |
| Oligonucleotide fo |
| Oligonucleotide fo |
| Shrimp polynucleot |
| Human prostate exp |
| Arabidopsis thalia |
| Drosophila melanog |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 448 | 18 | 0.9 | 553 | 22 | ABA17733 |
| | 449 | 18 | 0.9 | 553 | 22 | ABA17735 |
| | 450 | 18 | 0.9 | 600 | 22 | ABA61921 |
| | 451 | 18 | 0.9 | 600 | 22 | ABA29449 |
| | 452 | 18 | 0.9 | 600 | 22 | AAK10230 |
| | 453 | 18 | 0.9 | 600 | 22 | AAK36129 |
| | 454 | 18 | 0.9 | 600 | 22 | AAI17243 |
| | 455 | 18 | 0.9 | 600 | 22 | AAI41843 |
| | 456 | 18 | 0.9 | 600 | 24 | ABS10266 |
| c | 457 | 18 | 0.9 | 678 | 24 | ABN66378 |
| | 458 | 18 | 0.9 | 723 | 24 | ABQ65559 |
| c | 459 | 18 | 0.9 | 903 | 23 | ABL25669 |
| | 460 | 18 | 0.9 | 948 | 21 | AAC50054 |
| | 461 | 18 | 0.9 | 960 | 22 | ABA01504 |
| | 462 | 18 | 0.9 | 1110 | 23 | ABL12919 |
| c | 463 | 18 | 0.9 | 1125 | 23 | AAS91258 |
| c | 464 | 18 | 0.9 | 1134 | 22 | AAS34906 |
| | 465 | 18 | 0.9 | 1248 | 22 | ABA12555 |
| | 466 | 18 | 0.9 | 1265 | 21 | AAA50549 |
| | 467 | 18 | 0.9 | 1285 | 21 | AAC50552 |
| | 468 | 18 | 0.9 | 1287 | 21 | AAC34738 |
| c | 469 | 18 | 0.9 | 1296 | 23 | AAS55445 |
| c | 470 | 18 | 0.9 | 1296 | 23 | AAS55904 |
| | 471 | 18 | 0.9 | 1324 | 21 | AAC33357 |
| c | 472 | 18 | 0.9 | 1476 | 23 | ABL02079 |
| | 473 | 18 | 0.9 | 1503 | 24 | ABQ69112 |
| | 474 | 18 | 0.9 | 1515 | 24 | AAL47137 |
| | 475 | 18 | 0.9 | 1517 | 21 | AAC49293 |
| | 476 | 18 | 0.9 | 1523 | 21 | AAC37916 |
| c | 477 | 18 | 0.9 | 1550 | 22 | AAH55043 |
| | 478 | 18 | 0.9 | 1599 | 10 | AAN90733 |
| c | 479 | 18 | 0.9 | 1614 | 22 | ABA17863 |
| c | 480 | 18 | 0.9 | 1615 | 22 | ABA17864 |
| c | 481 | 18 | 0.9 | 1650 | 23 | ABL23323 |
| c | 482 | 18 | 0.9 | 1737 | 23 | ABL20395 |
| | 483 | 18 | 0.9 | 1747 | 23 | ABL03867 |
| c | 484 | 18 | 0.9 | 1749 | 24 | ABA91806 |
| c | 485 | 18 | 0.9 | 1760 | 22 | AAH15624 |
| c | 486 | 18 | 0.9 | 1815 | 21 | AAC76016 |
| | 487 | 18 | 0.9 | 1943 | 22 | AAK52621 |
| | 488 | 18 | 0.9 | 1982 | 10 | AAN90225 |
| | 489 | 18 | 0.9 | 1997 | 20 | AAX60931 |
| c | 490 | 18 | 0.9 | 2124 | 23 | ABL16559 |
| | 491 | 18 | 0.9 | 2185 | 24 | ABQ70770 |
| | 492 | 18 | 0.9 | 2204 | 19 | AAX24043 |
| | 493 | 18 | 0.9 | 2204 | 21 | AAC65469 |
| c | 494 | 18 | 0.9 | 2206 | 21 | AAA12390 |
| c | 495 | 18 | 0.9 | 2310 | 23 | ABL25668 |
| c | 496 | 18 | 0.9 | 2418 | 16 | AAQ99212 |
| | 497 | 18 | 0.9 | 2421 | 23 | AAS53323 |
| | 498 | 18 | 0.9 | 2460 | 24 | ABA94363 |
| c | 499 | 18 | 0.9 | 2574 | 22 | ABA89119 |
| | 500 | 18 | 0.9 | 2583 | 24 | ABQ70849 |
| c | 501 | 18 | 0.9 | 2609 | 23 | ABL24112 |
| | 502 | 18 | 0.9 | 2756 | 23 | ABL12176 |
| | 503 | 18 | 0.9 | 2914 | 23 | ABL24688 |
| | 504 | 18 | 0.9 | 2977 | 23 | ABL22502 |
| c | 505 | 18 | 0.9 | 2982 | 23 | ABL18589 |
| c | 506 | 18 | 0.9 | 2988 | 21 | AAF21257 |
| c | 507 | 18 | 0.9 | 2988 | 21 | AAA35135 |
| c | 508 | 18 | 0.9 | 3140 | 23 | ABL24110 |
| c | 509 | 18 | 0.9 | 3287 | 23 | ABL27298 |
| c | 510 | 18 | 0.9 | 3306 | 23 | ABL22716 |
| | 511 | 18 | 0.9 | 3385 | 23 | ABL15874 |
| c | 512 | 18 | 0.9 | 3493 | 23 | ABL02916 |
| | 513 | 18 | 0.9 | 3495 | 23 | ABL18978 |
| c | 514 | 18 | 0.9 | 3568 | 23 | ABL23930 |
| c | 515 | 18 | 0.9 | 3637 | 23 | ABL28887 |
| c | 516 | 18 | 0.9 | 3703 | 23 | ABL02078 |
| | 517 | 18 | 0.9 | 3812 | 23 | ABL23632 |
| | 518 | 18 | 0.9 | 3840 | 23 | ABL23322 |
| | 519 | 18 | 0.9 | 3891 | 20 | AAX60932 |
| c | 520 | 18 | 0.9 | 3926 | 22 | AAH54936 |

| |
|---|
| Human nervous syst |
| Human nervous syst |
| Human foetal liver |
| Probe #7915 for ge |
| Human brain expres |
| Human bone marrow |
| Probe #7176 for ge |
| Probe #10529 used |
| Human genome-deriv |
| Streptococcus poly |
| Arabidopsis thalia |
| Drosophila melanog |
| Arabidopsis thalia |
| Codon modified hum |
| Drosophila melanog |
| DNA encoding novel |
| cDNA encoding nove |
| Human nervous syst |
| DNA encoding bovin |
| Arabidopsis thalia |
| Arabidopsis thalia |
| Streptococcus pneu |
| Streptococcus pneu |
| Arabidopsis thalia |
| Drosophila melanog |
| Listeria monocytog |
| Pyrin domain conta |
| Arabidopsis thalia |
| Arabidopsis thalia |
| S. epidermidis gen |
| Genomic DNA from P |
| Human nervous syst |
| Human nervous syst |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Arabidopsis RNase |
| Human cDNA sequenc |
| Human ORFX ORF1571 |
| Human polynucleoti |
| Malaria-specific P |
| Human cell death p |
| Drosophila melanog |
| Listeria monocytog |
| Human core 2GnT DN |
| Human heart core 2 |
| Human interferon-b |
| Drosophila melanog |
| Recombinant human |
| Haemophilus influe |
| Human APRG polypep |
| Escherichia coli p |
| Listeria monocytog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Human low adenosin |
| Human adenosine re |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Drosophila melanog |
| Murine cell death |
| S. epidermidis gen |

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 521 | 18 | 0.9 | 3997 | 18 | AAT90167 | Promoter from clas |
| | 522 | 18 | 0.9 | 3999 | 20 | AAX28025 | Human IKAP coding |
| | 523 | 18 | 0.9 | 3999 | 22 | AAF29756 | Human IKAP coding |
| | 524 | 18 | 0.9 | 4045 | 22 | AAS46740 | Tumour suppressor |
| | 525 | 18 | 0.9 | 4138 | 22 | AAH54631 | S. epidermidis gen |
| c | 526 | 18 | 0.9 | 4150 | 23 | ABL03866 | Drosophila melanog |
| | 527 | 18 | 0.9 | 4347 | 23 | ABL21422 | Drosophila melanog |
| | 528 | 18 | 0.9 | 4360 | 23 | ABL20394 | Drosophila melanog |
| c | 529 | 18 | 0.9 | 4400 | 17 | AAT16151 | Apoptopic cerebral |
| | 530 | 18 | 0.9 | 4413 | 23 | ABL04492 | Drosophila melanog |
| | 531 | 18 | 0.9 | 4504 | 24 | ABQ70977 | Listeria monocytog |
| | 532 | 18 | 0.9 | 4561 | 21 | AAF22414 | Human secreted pro |
| c | 533 | 18 | 0.9 | 4581 | 23 | ABL12918 | Drosophila melanog |
| | 534 | 18 | 0.9 | 4640 | 23 | ABL18814 | Drosophila melanog |
| | 535 | 18 | 0.9 | 4677 | 23 | ABL15872 | Drosophila melanog |
| | 536 | 18 | 0.9 | 4788 | 22 | AAH14533 | Human cDNA sequenc |
| | 537 | 18 | 0.9 | 4794 | 23 | AAS68176 | DNA encoding novel |
| | 538 | 18 | 0.9 | 4794 | 23 | AAS69658 | DNA encoding novel |
| | 539 | 18 | 0.9 | 4794 | 23 | AAS74999 | DNA encoding novel |
| | 540 | 18 | 0.9 | 4794 | 23 | AAS84089 | DNA encoding novel |
| | 541 | 18 | 0.9 | 4795 | 23 | AAS74440 | DNA encoding novel |
| | 542 | 18 | 0.9 | 4796 | 23 | ABL12780 | Drosophila melanog |
| | 543 | 18 | 0.9 | 4802 | 23 | AAS72071 | DNA encoding novel |
| | 544 | 18 | 0.9 | 4803 | 22 | AAH81767 | Human differential |
| | 545 | 18 | 0.9 | 4803 | 23 | AAS78637 | DNA encoding novel |
| | 546 | 18 | 0.9 | 4985 | 23 | ABL01906 | Drosophila melanog |
| | 547 | 18 | 0.9 | 5185 | 24 | ABL33034 | Human immune syste |
| c | 548 | 18 | 0.9 | 5222 | 21 | AAA55964 | Human G713 5'-regu |
| c | 549 | 18 | 0.9 | 5234 | 23 | ABL11240 | Drosophila melanog |
| | 550 | 18 | 0.9 | 5313 | 24 | ABL32762 | Human immune syste |
| | 551 | 18 | 0.9 | 5357 | 23 | AAS73335 | DNA encoding novel |
| | 552 | 18 | 0.9 | 5413 | 22 | AAS46694 | Tumour suppressor |
| | 553 | 18 | 0.9 | 5416 | 24 | ABL33797 | Human immune syste |
| c | 554 | 18 | 0.9 | 5422 | 23 | ABL14321 | Drosophila melanog |
| c | 555 | 18 | 0.9 | 5559 | 24 | ABL33423 | Human immune syste |
| c | 556 | 18 | 0.9 | 5566 | 21 | AAA55967 | Human G713 encodin |
| | 557 | 18 | 0.9 | 5638 | 19 | AAV52350 | Streptococcus pneu |
| c | 558 | 18 | 0.9 | 5827 | 24 | ABK40053 | Human chemically p |
| c | 559 | 18 | 0.9 | 5849 | 19 | AAV33135 | Plasmodium berghei |
| | 560 | 18 | 0.9 | 5860 | 24 | ABL70524 | Chemically treated |
| | 561 | 18 | 0.9 | 5860 | 24 | AAS61373 | Human gene regulat |
| | 562 | 18 | 0.9 | 5860 | 24 | ABK31457 | Signal transductio |
| | 563 | 18 | 0.9 | 5930 | 24 | ABL32516 | Human immune syste |
| | 564 | 18 | 0.9 | 6134 | 22 | AAS46564 | Tumour suppressor |
| | 565 | 18 | 0.9 | 6147 | 24 | AAL45982 | Plasmid pSMICIP2s( |
| | 566 | 18 | 0.9 | 6163 | 22 | AAK51637 | Human polynucleoti |
| | 567 | 18 | 0.9 | 6274 | 24 | AAL41817 | Human glucosaminyl |
| | 568 | 18 | 0.9 | 6419 | 24 | ABL32266 | Human immune syste |
| | 569 | 18 | 0.9 | 6452 | 24 | ABN80275 | Human chemically m |
| | 570 | 18 | 0.9 | 6705 | 22 | AAF32778 | Human secreted pro |
| | 571 | 18 | 0.9 | 6731 | 24 | ABK39963 | Human chemically p |
| c | 572 | 18 | 0.9 | 6749 | 22 | AAS46526 | Tumour suppressor |
| c | 573 | 18 | 0.9 | 7145 | 24 | ABL92235 | Chemically treated |
| c | 574 | 18 | 0.9 | 7145 | 24 | AAD22322 | Chemically treated |
| c | 575 | 18 | 0.9 | 7195 | 22 | AAS45324 | Chemically pretrea |
| c | 576 | 18 | 0.9 | 7195 | 24 | ABK28165 | DNA transcription |
| c | 577 | 18 | 0.9 | 7269 | 23 | ABL19374 | Drosophila melanog |
| | 578 | 18 | 0.9 | 7306 | 24 | ABN80291 | Human chemically m |
| c | 579 | 18 | 0.9 | 7341 | 24 | ABQ67110 | Human angiogenesis |
| | 580 | 18 | 0.9 | 7422 | 23 | ABL14320 | Drosophila melanog |
| | 581 | 18 | 0.9 | 7491 | 24 | ABL33585 | Human immune syste |
| | 582 | 18 | 0.9 | 7589 | 24 | ABK28390 | DNA transcription |
| | 583 | 18 | 0.9 | 7823 | 22 | AAS45489 | Chemically pretrea |
| | 584 | 18 | 0.9 | 7823 | 24 | ABL34060 | Human immune syste |
| | 585 | 18 | 0.9 | 7823 | 24 | ABK28417 | DNA transcription |
| | 586 | 18 | 0.9 | 7823 | 24 | ABK31492 | Signal transductio |
| | 587 | 18 | 0.9 | 7890 | 24 | ABL70240 | Chemically treated |
| | 588 | 18 | 0.9 | 7890 | 24 | AAS61185 | Human gene regulat |
| | 589 | 18 | 0.9 | 8192 | 23 | ABL10252 | Drosophila melanog |
| c | 590 | 18 | 0.9 | 8227 | 24 | ABQ67126 | Human angiogenesis |
| c | 591 | 18 | 0.9 | 8318 | 20 | AAX20264 | Borrelia burgdorfe |
| | 592 | 18 | 0.9 | 8355 | 17 | AAT35524 | Human interferon-b |
| c | 593 | 18 | 0.9 | 8414 | 23 | ABL28886 | Drosophila melanog |
| c | 594 | 18 | 0.9 | 8446 | 23 | ABL03976 | Drosophila melanog |
| c | 595 | 18 | 0.9 | 9095 | 24 | ABK28448 | DNA transcription |
| c | 596 | 18 | 0.9 | 9186 | 23 | ABL24154 | Drosophila melanog |
| | 597 | 18 | 0.9 | 9265 | 24 | ABL34153 | Human immune syste |
| | 598 | 18 | 0.9 | 9265 | 24 | AAS63355 | Chemically pretrea |
| c | 599 | 18 | 0.9 | 9835 | 23 | ABL21524 | Drosophila melanog |
| c | 600 | 18 | 0.9 | 10120 | 23 | ABL18588 | Drosophila melanog |
| c | 601 | 18 | 0.9 | 10325 | 20 | AAX76516 | Plasmid containing |
| | 602 | 18 | 0.9 | 10339 | 22 | AAS40445 | DNA encoding human |
| | 603 | 18 | 0.9 | 10339 | 22 | AAL04059 | Human reproductive |
| c | 604 | 18 | 0.9 | 11416 | 24 | ABL70135 | Chemically treated |
| c | 605 | 18 | 0.9 | 11416 | 24 | ABL32118 | Human immune syste |
| c | 606 | 18 | 0.9 | 11416 | 24 | AAS61063 | Human gene regulat |
| c | 607 | 18 | 0.9 | 12393 | 24 | ABL33262 | Human immune syste |
| | 608 | 18 | 0.9 | 13427 | 24 | ABL33927 | Human immune syste |
| | 609 | 18 | 0.9 | 13814 | 24 | ABL33193 | Human immune syste |
| | 610 | 18 | 0.9 | 14551 | 24 | ABL34585 | Human metastasis a |
| c | 611 | 18 | 0.9 | 14919 | 22 | AAS46505 | Tumour suppressor |
| | 612 | 18 | 0.9 | 14987 | 24 | ABL32630 | Human immune syste |
| c | 613 | 18 | 0.9 | 15161 | 24 | ABL70458 | Chemically treated |
| c | 614 | 18 | 0.9 | 15161 | 24 | AAS61423 | Human gene regulat |
| c | 615 | 18 | 0.9 | 15306 | 22 | AAS45455 | Chemically pretrea |
| c | 616 | 18 | 0.9 | 15306 | 24 | ABK28310 | DNA transcription |
| | 617 | 18 | 0.9 | 15714 | 24 | ABQ67057 | Human angiogenesis |
| | 618 | 18 | 0.9 | 15714 | 24 | ABL33172 | Human immune syste |
| | 619 | 18 | 0.9 | 15767 | 24 | ABL33206 | Human immune syste |
| | 620 | 18 | 0.9 | 15767 | 24 | ABL34552 | Human metastasis a |
| c | 621 | 18 | 0.9 | 16373 | 24 | ABL32619 | Human immune syste |
| c | 622 | 18 | 0.9 | 16373 | 24 | AAD28383 | Human chemically t |
| c | 623 | 18 | 0.9 | 16946 | 22 | ABA20324 | Human nervous syst |
| c | 624 | 18 | 0.9 | 18434 | 24 | ABL34006 | Human immune syste |
| | 625 | 18 | 0.9 | 18683 | 24 | ABL54334 | Chemically treated |
| | 626 | 18 | 0.9 | 18683 | 24 | ABL32313 | Human immune syste |
| | 627 | 18 | 0.9 | 19082 | 24 | ABL32626 | Human immune syste |
| | 628 | 18 | 0.9 | 19702 | 19 | AAV52140 | Streptococcus pneu |
| | 629 | 18 | 0.9 | 20311 | 23 | ABL13796 | Drosophila melanog |
| c | 630 | 18 | 0.9 | 26678 | 23 | ABL02118 | Drosophila melanog |
| | 631 | 18 | 0.9 | 28360 | 23 | ABL06142 | Drosophila melanog |
| c | 632 | 18 | 0.9 | 28989 | 22 | ABA89112 | Escherichia coli p |
| c | 633 | 18 | 0.9 | 31214 | 23 | ABL16558 | Drosophila melanog |
| | 634 | 18 | 0.9 | 32392 | 24 | ABL56203 | AmEPV genome fragm |
| c | 635 | 18 | 0.9 | 36778 | 23 | ABL07548 | Drosophila melanog |
| c | 636 | 18 | 0.9 | 39265 | 24 | ABL52838 | Polynucleotide seq |
| c | 637 | 18 | 0.9 | 52691 | 22 | AAK84435 | Human immune/haema |
| c | 638 | 18 | 0.9 | 58407 | 19 | AAV21210 | Methanococcus jann |
| | 639 | 18 | 0.9 | 59967 | 23 | ABL15492 | Drosophila melanog |
| | 640 | 18 | 0.9 | 75899 | 24 | ABK85261 | Human genomic DNA |
| | 641 | 18 | 0.9 | 99960 | 21 | AAZ50905 | Human TBC-1 partia |
| | 642 | 18 | 0.9 | 139389 | 24 | ABK84795 | Human cDNA differe |
| c | 643 | 18 | 0.9 | 139389 | 24 | ABK84795 | Human cDNA differe |
| c | 644 | 18 | 0.9 | 220895 | 24 | ABK84798 | Human cDNA differe |
| | 645 | 18 | 0.9 | 319630 | 24 | ABQ67194 | Listeria innocua c |
| | 646 | 18 | 0.9 | 495269 | 24 | ABQ67195 | Listeria innocua c |
| | 647 | 18 | 0.9 | 513445 | 22 | AAI61373 | Soybean 318013 reg |
| | 648 | 18 | 0.9 | 910715 | 20 | AAX20248 | Borrelia burgdorfe |
| | 649 | 18 | 0.9 | 1664976 | 19 | AAV21209 | Methanococcus jann |
| c | 650 | 18 | 0.9 | 3011208 | 24 | ABQ69245 | Listeria innocua D |
| | 651 | 17 | 0.8 | 29 | 15 | AAQ58882 | Primer for amplify |
| c | 652 | 17 | 0.8 | 38 | 16 | AAQ99114 | cCIP DC oligo B -- |
| | 653 | 17 | 0.8 | 38 | 20 | AAZ06984 | Murine GABA B rece |
| | 654 | 17 | 0.8 | 38 | 22 | AAC91918 | Murine GABA-B-R1a |
| | 655 | 17 | 0.8 | 41 | 20 | AAX58073 | PCR primer for hum |
| | 656 | 17 | 0.8 | 41 | 21 | AAZ29439 | PCR primer JC139 f |
| | 657 | 17 | 0.8 | 50 | 20 | AAX58113 | PCR primer for hum |
| | 658 | 17 | 0.8 | 50 | 20 | AAX58091 | PCR primer for can |
| | 659 | 17 | 0.8 | 50 | 20 | AAX58075 | PCR primer for hum |
| | 660 | 17 | 0.8 | 51 | 22 | AAI76946 | Human silent SNP c |
| | 661 | 17 | 0.8 | 51 | 22 | AAI76947 | Human silent SNP c |
| | 662 | 17 | 0.8 | 60 | 22 | AAS45575 | B cell lymphoma CJ |
| | 663 | 17 | 0.8 | 60 | 22 | AAH20265 | CJ linker library |
| c | 664 | 17 | 0.8 | 65 | 24 | ABN31223 | Rat spliced transc |
| c | 665 | 17 | 0.8 | 116 | 21 | AAC12505 | Human secreted pro |
| | 666 | 17 | 0.8 | 125 | 16 | AAT25438 | Human gene signatu |

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 667 | 17 | 0.8 | 159 | 21 | AAC05820 | Human secreted pro |
| | 668 | 17 | 0.8 | 161 | 21 | AAC24191 | Human secreted pro |
| c | 669 | 17 | 0.8 | 189 | 22 | ABA51433 | Human breast cell |
| c | 670 | 17 | 0.8 | 189 | 22 | ABA69457 | Human foetal liver |
| c | 671 | 17 | 0.8 | 189 | 22 | ABA36385 | Probe #14851 for g |
| c | 672 | 17 | 0.8 | 189 | 22 | AAK17715 | Human brain expres |
| c | 673 | 17 | 0.8 | 189 | 22 | AAK43536 | Human bone marrow |
| c | 674 | 17 | 0.8 | 189 | 22 | AAI24317 | Probe #14250 for g |
| c | 675 | 17 | 0.8 | 189 | 22 | AAI49593 | Probe #18279 used |
| c | 676 | 17 | 0.8 | 189 | 22 | AAI09867 | Probe #9858 used t |
| c | 677 | 17 | 0.8 | 189 | 24 | ABS17665 | Human genome-deriv |
| | 678 | 17 | 0.8 | 208 | 23 | ABK42130 | Genomic sequence # |
| c | 679 | 17 | 0.8 | 218 | 22 | AAK58539 | Human immune/haema |
| | 680 | 17 | 0.8 | 223 | 6 | AAN50632 | Sequence which is |
| c | 681 | 17 | 0.8 | 228 | 13 | AAQ23094 | Antigen tc-10a gen |
| c | 682 | 17 | 0.8 | 235 | 23 | ABV16142 | Human prostate exp |
| c | 683 | 17 | 0.8 | 240 | 24 | ABL76340 | Corn tassel-derive |
| c | 684 | 17 | 0.8 | 246 | 21 | AAC23585 | Human secreted pro |
| c | 685 | 17 | 0.8 | 251 | 20 | AAV87555 | EST clone DW831. |
| | 686 | 17 | 0.8 | 261 | 22 | AAH93288 | Plasmodium falcipa |
| c | 687 | 17 | 0.8 | 276 | 22 | AAL02491 | Human reproductive |
| c | 688 | 17 | 0.8 | 288 | 23 | ABV12774 | Human prostate exp |
| c | 689 | 17 | 0.8 | 300 | 20 | AAX98384 | Human cancer cell |
| | 690 | 17 | 0.8 | 302 | 22 | AAH53139 | S. epidermidis ope |
| | 691 | 17 | 0.8 | 306 | 21 | AAA70221 | Plasmodium falcipa |
| | 692 | 17 | 0.8 | 309 | 22 | AAK53657 | Murine transport a |
| | 693 | 17 | 0.8 | 310 | 22 | AAH70592 | Human cervical can |
| | 694 | 17 | 0.8 | 314 | 21 | AAC31953 | Human secreted pro |
| | 695 | 17 | 0.8 | 334 | 22 | AAK77463 | Human immune/haema |
| | 696 | 17 | 0.8 | 334 | 22 | AAK77464 | Human immune/haema |
| c | 697 | 17 | 0.8 | 340 | 21 | AAC56095 | Eucalyptus grandis |
| c | 698 | 17 | 0.8 | 340 | 21 | AAC56462 | Eucalyptus grandis |
| c | 699 | 17 | 0.8 | 345 | 23 | ABL21343 | Drosophila melanog |
| c | 700 | 17 | 0.8 | 346 | 21 | AAC29784 | Human secreted pro |
| c | 701 | 17 | 0.8 | 351 | 23 | ABL15597 | Drosophila melanog |
| | 702 | 17 | 0.8 | 351 | 24 | ABN67138 | Streptococcus poly |
| c | 703 | 17 | 0.8 | 355 | 24 | ABL69904 | Pancreas cancer re |
| | 704 | 17 | 0.8 | 363 | 22 | AAH52782 | S. epidermidis ope |
| | 705 | 17 | 0.8 | 363 | 22 | AAH53025 | S. epidermidis ope |
| | 706 | 17 | 0.8 | 368 | 24 | ABN73683 | Bovine embryonic g |
| | 707 | 17 | 0.8 | 377 | 24 | ABL83372 | Human ovarian canc |
| | 708 | 17 | 0.8 | 378 | 22 | AAF68835 | Human lung tumour |
| | 709 | 17 | 0.8 | 378 | 24 | ABK38746 | cDNA encoding clon |
| c | 710 | 17 | 0.8 | 381 | 22 | AAI82405 | Human polynucleoti |
| c | 711 | 17 | 0.8 | 388 | 22 | AAI92145 | Human polynucleoti |
| c | 712 | 17 | 0.8 | 392 | 22 | AAL03785 | Human reproductive |
| c | 713 | 17 | 0.8 | 392 | 22 | AAL03786 | Human reproductive |
| c | 714 | 17 | 0.8 | 392 | 22 | AAK84136 | Human immune/haema |
| c | 715 | 17 | 0.8 | 392 | 22 | AAK84137 | Human immune/haema |
| c | 716 | 17 | 0.8 | 392 | 22 | AAI62602 | Human breast or ov |
| c | 717 | 17 | 0.8 | 392 | 22 | AAI62603 | Human breast or ov |
| | 718 | 17 | 0.8 | 393 | 22 | AAI85709 | Human polynucleoti |
| c | 719 | 17 | 0.8 | 394 | 23 | AAS64682 | DNA encoding novel |
| c | 720 | 17 | 0.8 | 394 | 23 | AAS67025 | DNA encoding novel |
| | 721 | 17 | 0.8 | 394 | 23 | AAS88139 | DNA encoding novel |
| | 722 | 17 | 0.8 | 396 | 22 | AAF94838 | Human ovarian canc |
| | 723 | 17 | 0.8 | 396 | 24 | ABT03105 | Human ovarian carc |
| | 724 | 17 | 0.8 | 396 | 24 | ABL48788 | Ovarian carcinoma |
| | 725 | 17 | 0.8 | 397 | 23 | AAS72700 | DNA encoding novel |
| | 726 | 17 | 0.8 | 401 | 21 | AAC65962 | Human lung cancer- |
| | 727 | 17 | 0.8 | 401 | 24 | ABL49181 | Human lung tumour |
| | 728 | 17 | 0.8 | 402 | 22 | AAL19980 | Human breast cance |
| | 729 | 17 | 0.8 | 404 | 22 | AAI81352 | Human polynucleoti |
| | 730 | 17 | 0.8 | 405 | 22 | AAI84469 | Human polynucleoti |
| | 731 | 17 | 0.8 | 407 | 22 | ABA58843 | Human foetal liver |
| | 732 | 17 | 0.8 | 407 | 22 | AAK07000 | Human brain expres |
| | 733 | 17 | 0.8 | 407 | 22 | AAK32741 | Human bone marrow |
| | 734 | 17 | 0.8 | 407 | 22 | AAI38554 | Probe #7240 used t |
| | 735 | 17 | 0.8 | 407 | 24 | ABS07539 | Human genome-deriv |
| | 736 | 17 | 0.8 | 415 | 21 | AAC02822 | Human secreted pro |
| c | 737 | 17 | 0.8 | 416 | 24 | ABL82362 | Human ovarian canc |
| c | 738 | 17 | 0.8 | 417 | 13 | AAQ23082 | Antigen tc-11e gen |
| | 739 | 17 | 0.8 | 420 | 23 | AAS65757 | DNA encoding novel |
| c | 740 | 17 | 0.8 | 443 | 22 | AAI90200 | Human polynucleoti |
| c | 741 | 17 | 0.8 | 444 | 22 | ABA42717 | Human breast cell |
| c | 742 | 17 | 0.8 | 444 | 22 | ABA53145 | Human foetal liver |
| c | 743 | 17 | 0.8 | 444 | 22 | AAK01392 | Human brain expres |
| c | 744 | 17 | 0.8 | 444 | 22 | AAI11475 | Probe #1408 for ge |
| c | 745 | 17 | 0.8 | 444 | 22 | AAI32750 | Probe #1436 used t |
| c | 746 | 17 | 0.8 | 444 | 22 | AAI01389 | Probe #1380 used t |
| | 747 | 17 | 0.8 | 452 | 22 | AAF44822 | RPP5-like protein |
| | 748 | 17 | 0.8 | 458 | 24 | ABQ56933 | Human colon cancer |
| c | 749 | 17 | 0.8 | 461 | 22 | AAK78570 | Human immune/haema |
| c | 750 | 17 | 0.8 | 461 | 22 | AAK78571 | Human immune/haema |
| c | 751 | 17 | 0.8 | 462 | 23 | ABL26941 | Drosophila melanog |
| | 752 | 17 | 0.8 | 476 | 24 | ABL37248 | Human colon tumour |
| c | 753 | 17 | 0.8 | 478 | 22 | AAK72992 | Human immune/haema |
| c | 754 | 17 | 0.8 | 478 | 22 | AAK72993 | Human immune/haema |
| c | 755 | 17 | 0.8 | 481 | 23 | ABV33903 | Human prostate exp |
| c | 756 | 17 | 0.8 | 481 | 23 | ABV42780 | Human prostate exp |
| c | 757 | 17 | 0.8 | 484 | 21 | AAC40989 | Zea mays DNA fragm |
| | 758 | 17 | 0.8 | 484 | 22 | AAI82987 | Human polynucleoti |
| c | 759 | 17 | 0.8 | 484 | 23 | AAS67838 | DNA encoding novel |
| c | 760 | 17 | 0.8 | 486 | 24 | ABL37717 | Human colon tumour |
| c | 761 | 17 | 0.8 | 489 | 22 | ABA46331 | Human breast cell |
| c | 762 | 17 | 0.8 | 489 | 22 | ABA53489 | Human foetal liver |
| c | 763 | 17 | 0.8 | 489 | 22 | ABA56892 | Human foetal liver |
| c | 764 | 17 | 0.8 | 489 | 22 | ABA23256 | Probe #1722 for ge |
| c | 765 | 17 | 0.8 | 489 | 22 | ABA26510 | Probe #4976 for ge |
| c | 766 | 17 | 0.8 | 489 | 22 | AAK01760 | Human brain expres |
| c | 767 | 17 | 0.8 | 489 | 22 | AAK04992 | Human brain expres |
| c | 768 | 17 | 0.8 | 489 | 22 | AAK27214 | Human bone marrow |
| c | 769 | 17 | 0.8 | 489 | 22 | AAK30526 | Human bone marrow |
| c | 770 | 17 | 0.8 | 489 | 22 | AAI11795 | Probe #1728 for ge |
| c | 771 | 17 | 0.8 | 489 | 22 | AAI15137 | Probe #5070 for ge |
| c | 772 | 17 | 0.8 | 489 | 22 | AAI33109 | Probe #1795 used t |
| c | 773 | 17 | 0.8 | 489 | 22 | AAI36471 | Probe #5157 used t |
| c | 774 | 17 | 0.8 | 489 | 22 | AAI01728 | Probe #1719 used t |
| c | 775 | 17 | 0.8 | 489 | 22 | AAI04888 | Probe #4879 used t |
| c | 776 | 17 | 0.8 | 489 | 24 | ABS05161 | Human genome-deriv |
| c | 777 | 17 | 0.8 | 494 | 23 | ABV10021 | Human prostate exp |
| | 778 | 17 | 0.8 | 496 | 22 | AAS35150 | Human cardiovascul |
| c | 779 | 17 | 0.8 | 496 | 23 | ABV53231 | Human prostate exp |
| | 780 | 17 | 0.8 | 497 | 23 | ABV59819 | Human prostate exp |
| c | 781 | 17 | 0.8 | 500 | 21 | AAC94494 | Cat flea hindgut a |
| | 782 | 17 | 0.8 | 500 | 22 | AAI88016 | Human polynucleoti |
| | 783 | 17 | 0.8 | 500 | 22 | AAI88019 | Human polynucleoti |
| c | 784 | 17 | 0.8 | 504 | 23 | ABV45940 | Human prostate exp |
| c | 785 | 17 | 0.8 | 505 | 23 | ABL28019 | Drosophila melanog |
| | 786 | 17 | 0.8 | 507 | 21 | AAA43249 | Xenopus secreted e |
| | 787 | 17 | 0.8 | 525 | 22 | AAH29466 | Drosophila melanog |
| | 788 | 17 | 0.8 | 535 | 22 | AAH13109 | Human cDNA clone ( |
| c | 789 | 17 | 0.8 | 546 | 22 | ABA62232 | Human foetal liver |
| c | 790 | 17 | 0.8 | 546 | 22 | ABA29584 | Probe #8050 for ge |
| c | 791 | 17 | 0.8 | 546 | 22 | AAK10563 | Human brain expres |
| c | 792 | 17 | 0.8 | 546 | 22 | AAK36461 | Human bone marrow |
| c | 793 | 17 | 0.8 | 546 | 22 | AAI17318 | Probe #7251 for ge |
| c | 794 | 17 | 0.8 | 546 | 22 | AAI42208 | Probe #10894 used |
| | 795 | 17 | 0.8 | 551 | 24 | AAI68822 | C. glutamicum ATCC |
| | 796 | 17 | 0.8 | 553 | 22 | ABA06651 | Human cDNA SEQ ID |
| | 797 | 17 | 0.8 | 553 | 22 | AAS41469 | cDNA encoding nove |
| c | 798 | 17 | 0.8 | 553 | 23 | ABV52025 | Human prostate exp |
| | 799 | 17 | 0.8 | 554 | 24 | ABK62748 | Rat sequence diffe |
| c | 800 | 17 | 0.8 | 560 | 22 | AAS30595 | DNA encoding novel |
| c | 801 | 17 | 0.8 | 560 | 22 | AAS28127 | Novel cDNA encodin |
| c | 802 | 17 | 0.8 | 562 | 23 | ABV17510 | Human prostate exp |
| c | 803 | 17 | 0.8 | 563 | 22 | AAH09542 | Human cDNA clone ( |
| c | 804 | 17 | 0.8 | 564 | 18 | AAV74801 | Staphylococcus aur |
| | 805 | 17 | 0.8 | 570 | 22 | AAK60727 | Human immune/haema |
| | 806 | 17 | 0.8 | 570 | 24 | ABN68241 | Streptococcus poly |
| | 807 | 17 | 0.8 | 572 | 20 | AAV80572 | Nucleic acid SEQ I |
| | 808 | 17 | 0.8 | 572 | 22 | ABA59673 | Human foetal liver |
| | 809 | 17 | 0.8 | 572 | 22 | AAK07943 | Human brain expres |
| | 810 | 17 | 0.8 | 572 | 22 | AAK33812 | Human bone marrow |
| | 811 | 17 | 0.8 | 572 | 22 | AAI39538 | Probe #8224 used t |
| c | 812 | 17 | 0.8 | 576 | 22 | AAK70216 | Human immune/haema |

| | | | | | | |
|---|---|---|---|---|---|---|
| c 813 | 17 | 0.8 | 576 | 22 | AAK70217 | Human immune/haema |
| c 814 | 17 | 0.8 | 580 | 22 | AAS30579 | DNA encoding novel |
| c 815 | 17 | 0.8 | 580 | 22 | AAL06716 | Human reproductive |
| c 816 | 17 | 0.8 | 580 | 22 | AAK76153 | Human immune/haema |
| 817 | 17 | 0.8 | 582 | 23 | ABV47242 | Human prostate exp |
| 818 | 17 | 0.8 | 583 | 24 | ABQ33514 | Oligonucleotide fo |
| c 819 | 17 | 0.8 | 583 | 24 | ABQ33515 | Oligonucleotide fo |
| c 820 | 17 | 0.8 | 587 | 22 | AAK59785 | Human immune/haema |
| 821 | 17 | 0.8 | 589 | 24 | ABQ29526 | Oligonucleotide fo |
| c 822 | 17 | 0.8 | 589 | 24 | ABQ29527 | Oligonucleotide fo |
| 823 | 17 | 0.8 | 603 | 20 | AAX20787 | Polynucleotide seq |
| 824 | 17 | 0.8 | 603 | 21 | AAC48462 | Arabidopsis thalia |
| 825 | 17 | 0.8 | 606 | 23 | ABV52086 | Human prostate exp |
| 826 | 17 | 0.8 | 607 | 20 | AAX21006 | Polynucleotide seq |
| c 827 | 17 | 0.8 | 609 | 23 | ABV58485 | Human prostate exp |
| c 828 | 17 | 0.8 | 620 | 23 | ABV54886 | Human prostate exp |
| 829 | 17 | 0.8 | 627 | 17 | AAT33280 | Keratinocyte growt |
| 830 | 17 | 0.8 | 627 | 19 | AAV48161 | Human fibroblast g |
| 831 | 17 | 0.8 | 627 | 19 | AAV28937 | Recombinant kerati |
| 832 | 17 | 0.8 | 627 | 19 | AAV11785 | Human keratinocyte |
| 833 | 17 | 0.8 | 627 | 19 | AAV19976 | Keratinocyte growt |
| 834 | 17 | 0.8 | 627 | 20 | AAZ11095 | Human keratinocyte |
| 835 | 17 | 0.8 | 627 | 20 | AAX85844 | DNA encoding human |
| 836 | 17 | 0.8 | 627 | 21 | AAA71203 | Human keratinocyte |
| 837 | 17 | 0.8 | 627 | 21 | AAZ52267 | Human fibroblast g |
| 838 | 17 | 0.8 | 627 | 22 | AAH28215 | Nucleotide sequenc |
| 839 | 17 | 0.8 | 627 | 22 | AAF31901 | Human keratinocyte |
| 840 | 17 | 0.8 | 627 | 22 | AAC92931 | Human keratinocyte |
| 841 | 17 | 0.8 | 627 | 24 | ABN62040 | Human cancer relat |
| 842 | 17 | 0.8 | 627 | 24 | ABL91712 | Human polynucleoti |
| 843 | 17 | 0.8 | 631 | 24 | ABQ66104 | Arabidopsis thalia |
| 844 | 17 | 0.8 | 637 | 24 | ABN60152 | Human cancer relat |
| 845 | 17 | 0.8 | 649 | 20 | AAX97883 | Human secreted pro |
| 846 | 17 | 0.8 | 651 | 22 | AAS46875 | Human G protein-co |
| 847 | 17 | 0.8 | 651 | 24 | ABK81653 | cDNA encoding nove |
| 848 | 17 | 0.8 | 690 | 18 | AAT77200 | Human fibroblast g |
| 849 | 17 | 0.8 | 690 | 20 | AAX03346 | cDNA encoding huma |
| 850 | 17 | 0.8 | 690 | 20 | AAX01743 | Human FGF-10 cDNA. |
| 851 | 17 | 0.8 | 690 | 20 | AAV82018 | Human fibroblast g |
| 852 | 17 | 0.8 | 692 | 22 | AAH06964 | Human cDNA clone ( |
| 853 | 17 | 0.8 | 700 | 22 | AAH92685 | Human inflammatory |
| c 854 | 17 | 0.8 | 737 | 20 | AAX98916 | Human validated ca |
| c 855 | 17 | 0.8 | 740 | 23 | ABV47304 | Human prostate exp |
| 856 | 17 | 0.8 | 741 | 24 | ABQ34748 | Oligonucleotide fo |
| c 857 | 17 | 0.8 | 741 | 24 | ABQ34749 | Oligonucleotide fo |
| 858 | 17 | 0.8 | 746 | 24 | ABQ25404 | Oligonucleotide fo |
| c 859 | 17 | 0.8 | 746 | 24 | ABQ25405 | Oligonucleotide fo |
| c 860 | 17 | 0.8 | 758 | 21 | AAZ32843 | Human chemokine be |
| c 861 | 17 | 0.8 | 765 | 23 | ABL24007 | Drosophila melanog |
| 862 | 17 | 0.8 | 773 | 24 | ABQ89708 | Human prostate exp |
| c 863 | 17 | 0.8 | 777 | 22 | AAH08575 | Human cDNA clone ( |
| c 864 | 17 | 0.8 | 801 | 23 | ABL28317 | Drosophila melanog |
| 865 | 17 | 0.8 | 809 | 13 | AAQ26809 | DNA encoding caGM- |
| 866 | 17 | 0.8 | 838 | 22 | AAK60311 | Human immune/haema |
| 867 | 17 | 0.8 | 844 | 24 | ABQ13916 | Oligonucleotide fo |
| c 868 | 17 | 0.8 | 844 | 24 | ABQ13917 | Oligonucleotide fo |
| c 869 | 17 | 0.8 | 858 | 22 | AAF22459 | Human breast cance |
| c 870 | 17 | 0.8 | 860 | 21 | AAA76271 | Maize glutathione- |
| c 871 | 17 | 0.8 | 863 | 22 | AAS60900 | Human cancer agent |
| 872 | 17 | 0.8 | 871 | 22 | AAS22585 | Human cDNA encodin |
| c 873 | 17 | 0.8 | 876 | 23 | AAS94119 | DNA encoding novel |
| c 874 | 17 | 0.8 | 882 | 23 | ABL21955 | Drosophila melanog |
| c 875 | 17 | 0.8 | 894 | 21 | AAA02492 | Human colon cancer |
| 876 | 17 | 0.8 | 909 | 21 | AAC76460 | Human ORFX ORF2015 |
| c 877 | 17 | 0.8 | 916 | 22 | AAI64161 | Maize defence-indu |
| 878 | 17 | 0.8 | 922 | 22 | AAS40817 | cDNA encoding nove |
| 879 | 17 | 0.8 | 922 | 22 | AAS41445 | cDNA encoding nove |
| 880 | 17 | 0.8 | 926 | 23 | AAS82847 | DNA encoding novel |
| 881 | 17 | 0.8 | 927 | 23 | ABL27953 | Drosophila melanog |
| 882 | 17 | 0.8 | 939 | 22 | AAH64821 | Human secreted pro |
| c 883 | 17 | 0.8 | 939 | 23 | ABL28527 | Drosophila melanog |
| 884 | 17 | 0.8 | 948 | 22 | AAF71440 | Corynebacterium gl |
| 885 | 17 | 0.8 | 948 | 22 | AAF71441 | Corynebacterium gl |
| c 886 | 17 | 0.8 | 966 | 18 | AAT87430 | Clone H174-10. Ho |
| 887 | 17 | 0.8 | 974 | 24 | ABQ17204 | Oligonucleotide fo |
| c 888 | 17 | 0.8 | 974 | 24 | ABQ17205 | Oligonucleotide fo |
| 889 | 17 | 0.8 | 1001 | 21 | AAC57541 | Arachidonic acid m |
| 890 | 17 | 0.8 | 1001 | 24 | ABL90125 | Human polynucleoti |
| 891 | 17 | 0.8 | 1006 | 21 | AAZ97042 | Human secreted pro |
| 892 | 17 | 0.8 | 1008 | 24 | ABK72761 | Bacillus lichenifo |
| 893 | 17 | 0.8 | 1022 | 23 | ABV13164 | Human prostate exp |
| c 894 | 17 | 0.8 | 1024 | 20 | AAX99093 | Human cancer cell |
| 895 | 17 | 0.8 | 1024 | 22 | AAH99809 | Human protein enco |
| 896 | 17 | 0.8 | 1026 | 24 | ABQ42256 | Oligonucleotide fo |
| c 897 | 17 | 0.8 | 1026 | 24 | ABQ42257 | Oligonucleotide fo |
| c 898 | 17 | 0.8 | 1061 | 21 | AAC53513 | Arabidopsis thalia |
| c 899 | 17 | 0.8 | 1070 | 23 | ABL16775 | Drosophila melanog |
| 900 | 17 | 0.8 | 1079 | 24 | ABQ27778 | Oligonucleotide fo |
| c 901 | 17 | 0.8 | 1079 | 24 | ABQ27779 | Oligonucleotide fo |
| c 902 | 17 | 0.8 | 1081 | 20 | AAZ23913 | Human SBHUNC50 DNA |
| c 903 | 17 | 0.8 | 1100 | 20 | AAZ23914 | Human SBHUNC50 DNA |
| c 904 | 17 | 0.8 | 1120 | 21 | AAF16160 | Human prostate can |
| 905 | 17 | 0.8 | 1124 | 24 | ABN98320 | Arabidopsis thalia |
| c 906 | 17 | 0.8 | 1134 | 21 | AAC53300 | Arabidopsis thalia |
| 907 | 17 | 0.8 | 1139 | 24 | AAD33702 | Human secreted pro |
| c 908 | 17 | 0.8 | 1163 | 21 | AAC34675 | Arabidopsis thalia |
| 909 | 17 | 0.8 | 1165 | 22 | ABA09033 | Human secreted pro |
| c 910 | 17 | 0.8 | 1187 | 21 | AAC81029 | Human secreted pro |
| 911 | 17 | 0.8 | 1189 | 22 | AAH33442 | Human colon cancer |
| c 912 | 17 | 0.8 | 1194 | 22 | AAS02224 | Corn Wuschel (WUS) |
| 913 | 17 | 0.8 | 1210 | 22 | AAD03369 | Human 103 gene. H |
| c 914 | 17 | 0.8 | 1214 | 19 | AAV33192 | Secreted protein C |
| c 915 | 17 | 0.8 | 1219 | 20 | AAX20441 | Human secreted pro |
| c 916 | 17 | 0.8 | 1229 | 21 | AAC36646 | Arabidopsis thalia |
| c 917 | 17 | 0.8 | 1229 | 21 | AAC49307 | Arabidopsis thalia |
| 918 | 17 | 0.8 | 1261 | 22 | AAI59910 | Human polynucleoti |
| 919 | 17 | 0.8 | 1263 | 24 | ABN91505 | Staphylococcus epi |
| 920 | 17 | 0.8 | 1265 | 19 | AAV28473 | Murine interleukin |
| 921 | 17 | 0.8 | 1271 | 24 | ABQ70445 | Listeria monocytog |
| 922 | 17 | 0.8 | 1282 | 20 | AAX18178 | Canine full length |
| c 923 | 17 | 0.8 | 1282 | 22 | AAS26109 | Human cDNA encodin |
| 924 | 17 | 0.8 | 1284 | 24 | ABL34363 | Human immune syste |
| 925 | 17 | 0.8 | 1316 | 23 | AAS82850 | DNA encoding novel |
| 926 | 17 | 0.8 | 1347 | 21 | AAA75617 | Nucleotide sequenc |
| 927 | 17 | 0.8 | 1347 | 24 | AAS20732 | Human zalphal1 Lig |
| c 928 | 17 | 0.8 | 1354 | 18 | AAT87431 | Clone H174-43. Ho |
| c 929 | 17 | 0.8 | 1354 | 21 | AAA30224 | Human non-ELR CXC |
| 930 | 17 | 0.8 | 1357 | 22 | AAI71657 | Human ST2 coding s |
| 931 | 17 | 0.8 | 1357 | 22 | AAD03367 | DNA encoding secre |
| 932 | 17 | 0.8 | 1357 | 22 | AAC92159 | Human 103 gene nuc |
| 933 | 17 | 0.8 | 1358 | 13 | AAQ24482 | Stearoyl-ACP-desat |
| c 934 | 17 | 0.8 | 1370 | 23 | ABL15803 | Drosophila melanog |
| c 935 | 17 | 0.8 | 1371 | 20 | AAX33332 | Human CXC chemokin |
| 936 | 17 | 0.8 | 1373 | 20 | AAX04848 | Human lysophosphat |
| c 937 | 17 | 0.8 | 1380 | 22 | AAH65688 | C glutamicum codin |
| 938 | 17 | 0.8 | 1383 | 21 | AAA51059 | Human LPAAT-beta c |
| 939 | 17 | 0.8 | 1383 | 21 | AAA39292 | Human lysophosphat |
| 940 | 17 | 0.8 | 1383 | 22 | AAC62351 | Nucleotide sequenc |
| 941 | 17 | 0.8 | 1383 | 24 | ABL61913 | Colon adenocarcino |
| 942 | 17 | 0.8 | 1383 | 24 | ABL67997 | Ovary cancer relat |
| 943 | 17 | 0.8 | 1383 | 24 | AAD24422 | Human LPAAT beta p |
| 944 | 17 | 0.8 | 1420 | 22 | ABA19975 | Human nervous syst |
| 945 | 17 | 0.8 | 1421 | 22 | ABA19974 | Human nervous syst |
| c 946 | 17 | 0.8 | 1427 | 22 | AAC86680 | DNA encoding a yea |
| c 947 | 17 | 0.8 | 1437 | 23 | ABL10183 | Drosophila melanog |
| c 948 | 17 | 0.8 | 1473 | 20 | AAZ28295 | Rat neuronal immed |
| c 949 | 17 | 0.8 | 1493 | 22 | AAK67730 | Human immune/haema |
| c 950 | 17 | 0.8 | 1503 | 24 | ABK34627 | Human cDNA for nov |
| c 951 | 17 | 0.8 | 1510 | 23 | ABL29879 | Drosophila melanog |
| c 952 | 17 | 0.8 | 1512 | 21 | AAA64513 | Nucleotide sequenc |
| 953 | 17 | 0.8 | 1522 | 24 | ABL63342 | Breast cancer rela |
| 954 | 17 | 0.8 | 1522 | 24 | ABL64142 | Stomach cancer rel |
| 955 | 17 | 0.8 | 1527 | 18 | AAT85928 | DNA encoding lysop |
| 956 | 17 | 0.8 | 1529 | 23 | ABL02155 | Drosophila melanog |
| c 957 | 17 | 0.8 | 1539 | 24 | ABK50986 | DNA encoding absci |
| c 958 | 17 | 0.8 | 1561 | 22 | AAI70030 | Partial pea END1 g |

| | | | | | | |
|---|---|---|---|---|---|---|
| 959 | 17 | 0.8 | 1566 | 24 | ABL90607 | Human polynucleoti |
| c 960 | 17 | 0.8 | 1569 | 23 | AAS93176 | DNA encoding novel |
| c 961 | 17 | 0.8 | 1569 | 23 | AAS93252 | DNA encoding novel |
| 962 | 17 | 0.8 | 1580 | 24 | ABK48902 | Novel human kallik |
| 963 | 17 | 0.8 | 1590 | 24 | ABK31746 | DNA encoding novel |
| 964 | 17 | 0.8 | 1592 | 24 | ABL90295 | Human polynucleoti |
| c 965 | 17 | 0.8 | 1598 | 23 | ABL09793 | Drosophila melanog |
| c 966 | 17 | 0.8 | 1614 | 21 | AAA64512 | Nucleotide sequenc |
| c 967 | 17 | 0.8 | 1621 | 22 | AAF61005 | P. putida KT2440-a |
| 968 | 17 | 0.8 | 1636 | 23 | ABL08565 | Drosophila melanog |
| 969 | 17 | 0.8 | 1639 | 20 | AAV80562 | Human lysophosphat |
| 970 | 17 | 0.8 | 1659 | 22 | AAH17187 | Human cDNA sequenc |
| 971 | 17 | 0.8 | 1680 | 22 | AAD03368 | DNA encoding varia |
| c 972 | 17 | 0.8 | 1692 | 21 | AAA64514 | Nucleotide sequenc |
| c 973 | 17 | 0.8 | 1695 | 21 | AAC41990 | Arabidopsis thalia |
| c 974 | 17 | 0.8 | 1722 | 21 | AAA64515 | Nucleotide sequenc |
| 975 | 17 | 0.8 | 1761 | 24 | ABQ31702 | Oligonucleotide fo |
| c 976 | 17 | 0.8 | 1761 | 24 | ABQ31703 | Oligonucleotide fo |
| c 977 | 17 | 0.8 | 1791 | 21 | AAA64509 | cDNA sequence enco |
| c 978 | 17 | 0.8 | 1791 | 24 | ABN96888 | Gene #3386 used to |
| c 979 | 17 | 0.8 | 1795 | 22 | AAI93828 | Human polynucleoti |
| c 980 | 17 | 0.8 | 1812 | 23 | ABL23633 | Drosophila melanog |
| c 981 | 17 | 0.8 | 1820 | 21 | AAZ46048 | cDNA sequence of a |
| 982 | 17 | 0.8 | 1820 | 22 | AAH28336 | Nucleotide sequenc |
| 983 | 17 | 0.8 | 1829 | 24 | ABL34409 | Human immune syste |
| c 984 | 17 | 0.8 | 1830 | 24 | ABL56243 | AmEPV metalloprote |
| c 985 | 17 | 0.8 | 1868 | 23 | ABL21045 | Drosophila melanog |
| c 986 | 17 | 0.8 | 1869 | 24 | ABK34748 | Human cDNA for nov |
| c 987 | 17 | 0.8 | 1879 | 23 | ABL05443 | Drosophila melanog |
| c 988 | 17 | 0.8 | 1895 | 22 | AAK75797 | Human immune/haema |
| 989 | 17 | 0.8 | 1896 | 22 | AAF61374 | Potato chloroplast |
| 990 | 17 | 0.8 | 1902 | 24 | ABK62573 | Rat sequence diffe |
| c 991 | 17 | 0.8 | 1907 | 23 | ABL11969 | Drosophila melanog |
| 992 | 17 | 0.8 | 1917 | 23 | ABL18115 | Drosophila melanog |
| c 993 | 17 | 0.8 | 1924 | 22 | AAF59598 | Human cell cycle a |
| c 994 | 17 | 0.8 | 1931 | 21 | AAC78060 | Human cancer assoc |
| c 995 | 17 | 0.8 | 1935 | 23 | ABL06313 | Drosophila melanog |
| 996 | 17 | 0.8 | 1936 | 20 | AAV74263 | Human heart muscle |
| 997 | 17 | 0.8 | 1991 | 22 | AAK68238 | Human immune/haema |
| c 998 | 17 | 0.8 | 2007 | 19 | AAV70959 | DNA encoding maize |
| c 999 | 17 | 0.8 | 2007 | 19 | AAV29754 | Zea mays soluble s |
| 1000 | 17 | 0.8 | 2058 | 22 | AAI71658 | Human coding seque |

ALIGNMENTS

```
RESULT 1
AAX87914
ID   AAX87914 standard; cDNA; 2102 BP.
XX
AC   AAX87914;
XX
DT   22-NOV-1999  (first entry)
XX
DE   Human CD55 tumour associated antigen cDNA.
XX
KW   CD55; decay accelerating factor; DAF; tumour associated antigen;
KW   791Tgp72; colorectal cancer; breast cancer; ovary cancer;
KW   osteosarcoma; vaccine; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1211
FT                   /*tag= a
FT   sig_peptide     66..167
FT                   /*tag= b
FT   mat_peptide     168..1208
FT                   /*tag= c
XX
PN   WO9943800-A1.
XX
PD   02-SEP-1999.
XX
PF   26-FEB-1999;   99WO-GB00582.
XX
PR   26-FEB-1998;   98GB-0004065.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Durrant LG,  Spendlove I;
XX
DR   WPI; 1999-540585/45.
DR   P-PSDB; AAY31740.
XX
PT   Cancer vaccine containing CD55 family polypeptide, to induce at
PT   least one of T helper, cytotoxic T cell or natural killer immune
PT   response
XX
PS   Claim 14; Fig 10; P 82pp; English.
XX
CC   This is the nucleotide sequence of cDNA coding for human CD55 (see
CC   AAY31740) or decay accelerating factor (DAF), which is over-expressed
CC   on a wide range of solid tumours.  A claimed cancer vaccine
CC   comprises a polypeptide of the CD55 family, including full-length
CC   CD55 or the new tumour associated antigen 791Tgp72, or an antigen,
CC   polypeptide, fragment or derivative of CD55 or 791Tgp72.  Claimed
CC   cancer vaccines also include nucleic acids encoding CD55 or 791Tgp72
CC   antigen, polypeptide, fragment or derivative.  Claimed methods of
CC   treating a cancer patient involve administering the cancer vaccine.
CC   CD55 and 791Tgp72 have identical amino acid sequences and are
CC   encoded by cDNA which is identical over the entire coding region,
CC   through differences exist in the 5' and 3' non-coding regions and
CC   in the glycosylation pattern of the proteins.  The cancer vaccines
CC   induce at least one of T helper, cytotoxic T cell or natural killer
CC   immune responses, possibly also production of neutralizing
CC   antibodies and complement-mediated lysis.  They are useful for
CC   treating e.g. colorectal, breast or ovarian cancer or osteosarcoma,
CC   where these are associated with overexpression of 791Tgp72.
XX
SQ   Sequence 2102 BP; 661 A; 419 C; 445 G; 577 T; 0 other;

  Query Match           100.0%;  Score 2102;  DB 20;  Length 2102;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 2102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
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Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260

Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380

Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620

Qy   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680

Qy   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740

Qy   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800

Qy   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860

Qy   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920

Qy   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980

Qy   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040

Qy   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100

Qy   2101 GT 2102
          ||
Db   2101 GT 2102
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RESULT 2
ABK83991
ID  ABK83991 standard; cDNA; 2102 BP.
XX
AC  ABK83991;
XX
DT  14-AUG-2002  (first entry)
XX
DE  Human cDNA differentially expressed in granulocytic cells #562.
XX
KW  Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW  viral infection; parasitic infection; protozoal infection;
KW  fungal infection; sterile inflammatory disease; psoriasis;
KW  rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW  cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW  adult respiratory distress syndrome; inflammatory bowel disease;
KW  Crohn's disease; ulcerative colitis; periodontal disease;
KW  granulocyte activation; chronic inflammation; allergy.
XX
OS  Homo sapiens.
XX
PN  WO200228999-A2.
XX
PD  11-APR-2002.
XX
PF  03-OCT-2001; 2001WO-US30821.
XX
PR  03-OCT-2000; 2000US-237189P.
XX
PA  (GENE-) GENE LOGIC INC.

XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S,. Vockley J;
XX
DR WPI; 2002-435328/46.
XX
PT Detecting granulocyte activation by detecting differential expression
PT of genes associated with granulocyte activation, which serves as
PT diagnostic markers that is useful for monitoring disease states and
PT drug toxicity -
XX
PS Claim 1; SEQ ID No 562; 114pp; English.
XX
CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing
CC the expression level to an expression level in an unactivated
CC GC, where differential expression of Gs is indicative of GCA.
CC Also included are modulating (M2) GA by contacting GC with an agent
CC that alters the expression of at least one gene in Gs; (2) screening (M3)
CC for an agent capable of modulating GCA or an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease using the
CC gene expression profile; (3) detecting (M4) an inflammation (especially
CC chronic) in a tissue, an allergic response in a subject, exposure of a
CC subject to a pathogen or sterile inflammatory disease, by detecting the
CC level of expression in a sample of the tissue of gene(s) from Gs, where
CC the level of expression of the gene is indicative of inflammation;
CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
CC an allergic response in a subject, exposure of a subject to a pathogen
CC or sterile inflammatory disease, by contacting a tissue having
CC inflammation with an agent that modulates the expression of gene(s)
CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
CC modulating GA; M3 is useful for screening an agent capable of modulating
CC GCA preferably in an inflammation in a tissue; M4 is useful for
CC detecting an inflammation (especially chronic) in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
CC reperfusion injury, ARDS, adult respiratory distress syndrome,
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC periodontal disease; also bacterial infection, viral infection,
CC parasitic infection, protozoal infection, fungal infection and M5 is
CC useful for treating one of the above conditions. The present
CC sequence represents a gene differentially expressed in granulocytes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2102 BP; 661 A; 419 C; 445 G; 577 T; 0 other;

Query Match 100.0%; Score 2102; DB 24; Length 2102;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
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Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
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Db     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
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Db     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
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Db     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
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Db     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
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Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
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Db     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Db     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
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Qy    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
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Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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Qy    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAAATACACACAAGTATACAGACTGTTCCT 1260
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Qy    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
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Qy    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
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Db    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
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Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
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Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
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Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620
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Db   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620

Qy   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680
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Db   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680

Qy   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740
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Db   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800

Qy   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860
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Db   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860

Qy   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920
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Qy   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
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Qy   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
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Db   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100

Qy   2101 GT 2102
          ||
Db   2101 GT 2102
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RESULT 3
ABL65229
ID  ABL65229 standard; DNA; 2102 BP.
XX
AC  ABL65229;
XX
DT  15-MAY-2002 (first entry)
XX
DE  Lung cancer related gene sequence SEQ ID NO:3566.
XX
KW  Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW  stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW  cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW  gene; ds.
XX
OS  Homo sapiens.
XX
PN  WO200194629-A2.
XX
PD  13-DEC-2001.
XX
PF  30-MAY-2001; 2001WO-US10838.
XX
PR  05-JUN-2000; 2000US-209473P.
PR  05-JUN-2000; 2000US-209531P.
PR  18-SEP-2000; 2000US-233133P.
PR  18-SEP-2000; 2000US-233617P.
PR  20-SEP-2000; 2000US-234009P.
PR  20-SEP-2000; 2000US-234034P.
PR  20-SEP-2000; 2000US-234052P.
PR  22-SEP-2000; 2000US-234509P.
PR  22-SEP-2000; 2000US-234567P.
PR  25-SEP-2000; 2000US-234923P.
PR  25-SEP-2000; 2000US-234924P.
PR  25-SEP-2000; 2000US-235077P.
PR  25-SEP-2000; 2000US-235082P.
PR  25-SEP-2000; 2000US-235134P.
PR  25-SEP-2000; 2000US-235280P.
PR  26-SEP-2000; 2000US-235637P.
PR  26-SEP-2000; 2000US-235638P.
PR  27-SEP-2000; 2000US-235711P.
PR  27-SEP-2000; 2000US-235720P.
PR  27-SEP-2000; 2000US-235840P.
PR  27-SEP-2000; 2000US-235863P.
PR  28-SEP-2000; 2000US-236028P.
PR  28-SEP-2000; 2000US-236032P.
PR  28-SEP-2000; 2000US-236033P.
PR  28-SEP-2000; 2000US-236034P.
PR  28-SEP-2000; 2000US-236109P.
PR  28-SEP-2000; 2000US-236111P.
PR  29-SEP-2000; 2000US-236842P.
PR  29-SEP-2000; 2000US-236891P.
PR  02-OCT-2000; 2000US-237172P.
PR  02-OCT-2000; 2000US-237173P.
PR  02-OCT-2000; 2000US-237278P.
PR  02-OCT-2000; 2000US-237294P.
PR  02-OCT-2000; 2000US-237295P.
PR  02-OCT-2000; 2000US-237316P.
PR  03-OCT-2000; 2000US-237425P.
PR  03-OCT-2000; 2000US-237598P.
PR  03-OCT-2000; 2000US-237604P.
PR  03-OCT-2000; 2000US-237606P.
PR  03-OCT-2000; 2000US-237608P.
PR  01-NOV-2000; 2000US-244867P.
PR  01-NOV-2000; 2000US-245084P.
XX
PA  (AVAL-) AVALON PHARM.
XX
PI  Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI  Soppet DR, Weaver Z;
XX
DR  WPI; 2002-188264/24.
XX
PT  Screening for anti-neoplastic agent involves exposing cells to a
PT  chemical agent to be tested for anti-neoplastic activity, and
PT  determining a change in expression of a gene of a signature gene set -
XX
PS  Claim 1; SEQ ID 3566; 44pp; English.
XX
CC  The present invention describes a method (M1) for screening for an
CC  anti-neoplastic agent. The method involves exposing cells to a chemical
CC  agent to be tested for anti-neoplastic activity, determining a change in
CC  expression of at least one gene (I) of a signature gene set, where (I)
CC  comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC  to ABL70110), or is at least 95% identical to (S), where a change in
CC  expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC  activity and can be used in gene therapy. M1 can be used for screening
CC  an anti-neoplastic agent, and can be used for producing a product which
CC  is the data collected with respect to the anti-neoplastic agent as a
CC  result of M1, and the data is sufficient to convey the chemical
CC  structure and/or properties of the agent. M1 can be used in the
CC  treatment of cancer such as colon, breast, stomach, lung, thyroid,

CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,
CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
CC carcinoma, papillary carcinoma and Wilm's tumour.
XX
SQ Sequence 2102 BP; 661 A; 419 C; 445 G; 577 T; 0 other;

Query Match 100.0%; Score 2102; DB 24; Length 2102;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
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Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
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Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
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Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
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Db     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
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Db     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
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Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
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Db     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
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Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
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Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
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Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy    1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy    1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620

Qy    1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680

Qy    1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740

Qy    1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800

Qy    1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860

Qy    1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920

Qy    1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980

Qy    1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
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Qy    2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100

Qy    2101 GT 2102
           ||
Db    2101 GT 2102
```

RESULT 4
AAH34999
ID AAH34999 standard; cDNA; 2302 BP.
XX
AC AAH34999;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2081.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 1; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG75594.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3567; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 2302 BP; 727 A; 486 C; 479 G; 609 T; 1 other;

Query Match 100.0%; Score 2102; DB 22; Length 2302;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     169 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 228

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     229 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 288

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     289 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 348

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     349 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 408

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     409 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 468

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     469 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 528

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     529 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 588

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     589 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 648

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     649 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 708

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     709 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 768

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     769 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 828

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     829 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 888

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     889 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 948

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     949 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 1008

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1009 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 1068

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1069 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 1128

Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1129 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1188

Qy    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1189 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1248

Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1249 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1308

Qy   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1368

Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1428

Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1488

Qy   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1548

Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1608

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1668

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1728

Qy   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1729 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1788

Qy   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1789 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1848

Qy   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1849 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1908

Qy   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1909 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1968

Qy   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1969 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 2028

Qy   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2029 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 2088

Qy   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2089 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 2148

Qy   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2149 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2208

Qy   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2209 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2268

Qy   2101 GT 2102
          ||
Db   2269 GT 2270
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RESULT 5
AAH23076

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ID   AAH23076 standard; DNA; 2263 BP.
XX
AC   AAH23076;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Osteoarthritis tissue-derived nucleic acid sequence #6.
XX
KW   Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;
KW   wound healing; osteopathic; anti-arthritic, anti-inflammatory;
KW   vulnerary; antibacterial; antiallergic; ds.
XX
OS   Homo sapiens.
XX
PN   WO200153531-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US00016.
XX
PR   18-JAN-2000; 2000US-0176523.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Phippard D,  Vasanthakamur G,  Dotson S,  Ma X;
XX
DR   WPI; 2001-451914/48.
XX
PT   Substantially purified protein, polypeptide or their fragments, used to
PT   identify a biologically active compound or composition and treat
PT   mammalian osteoarthritis  -
XX
PS   Claim 1; Page 93-95; 144pp; English.
XX
CC   Sequences AAH23071-23152 represent nucleic acid sequences derived from
CC   osteoarthritis tissues. The sequences are useful as probes and for the
CC   diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides
CC   and polypeptides of the invention are useful for generating diagnostic
CC   reagents, as targets for small molecule drug development, generation of
CC   therapeutics, and cloning genes. Specific antibodies are used to generate
CC   enzyme linked immunosorbent assays for detection of osteoarthritis. The
CC   invented molecules can be used to treat osteoarthritis or to analyse the
CC   disease-modifying activity of osteoarthritis drugs. Other disorders
CC   treatable using the nucleic acid sequences include atopic, inflammatory
CC   and infectious disorders e.g. Crohn's disease and sepsis, and wound
CC   healing.
XX
SQ   Sequence 2263 BP; 706 A; 475 C; 474 G; 607 T; 1 other;
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  Query Match             93.6%;  Score 1968;  DB 22;  Length 2263;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2088;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy      15 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 74
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     161 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 220

Qy      75 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     221 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 280

Qy     135 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 194
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     281 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 340

Qy     195 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     341 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 400

Qy     255 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     401 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 460
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Qy    315 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 520

Qy    375 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 580

Qy    435 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 640

Qy    495 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    641 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 700

Qy    555 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 760

Qy    615 GCAACCAT-CTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 673
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 GCAACCATGCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 820

Qy    674 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 880

Qy    734 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    881 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 940

Qy    794 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    941 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 1000

Qy    854 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1001 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1060

Qy    914 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1061 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1120

Qy    974 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1121 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1180

Qy   1034 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1181 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1240

Qy   1094 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1241 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1300

Qy   1154 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1213
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1301 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1360

Qy   1214 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1273
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1361 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1420

Qy   1274 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1333
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1421 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1480

Qy   1334 CTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCAC 1393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1481 CTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCAC 1540

Qy   1394 ATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCC 1453
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1541 ATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCC 1600

Qy   1454 TTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGA 1513
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1601 TTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGA 1660

Qy   1514 AAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGG 1573
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1661 AAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGG 1720

Qy   1574 AAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCT 1633
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1721 AAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCT 1780

Qy   1634 CTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAA 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1781 CTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAA 1840

Qy   1694 GGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAA 1753
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1841 GGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAA 1900

Qy   1754 CCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGT 1813
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1901 CCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGT 1960

Qy   1814 TGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTA 1873
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1961 TGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTA 2020

Qy   1874 AAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATC 1933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2021 AAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATC 2080

Qy   1934 GAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATT 1993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2081 GAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATT 2140

Qy   1994 TATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGA 2053
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2141 TATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGA 2200

Qy   2054 AGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2102
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   2201 AGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2249
```

RESULT 6
AAQ79863
ID  AAQ79863 standard; cDNA; 2115 BP.
XX
AC  AAQ79863;
XX
DT  23-JUL-1995  (first entry)
XX
DE  Decay accelerating factor cDNA.
XX
KW  Decay accelerating factor; DAF; mDAF; fusion protein; liposome;
KW  cell targeting; glycophosphatidylinositol; GPI; drug delivery; ds.
XX
OS  Homo sapiens.
XX
FH  Key             Location/Qualifiers
FT  CDS             66..1211
FT                  /*tag=  a
FT  sig_peptide     66..167
FT                  /*tag=  b
FT  mat_peptide     168..1208
FT                  /*tag=  c
FT                  /product= mature mDAF protein
XX
PN  US5374548-A.

XX
PD 20-DEC-1994.
XX
PF 02-MAY-1986; 86US-0859107.
XX
PR 02-MAY-1986; 86US-0859107.
PR 06-AUG-1987; 87US-0083757.
PR 19-DEC-1991; 91US-0811048.
PR 12-FEB-1993; 93US-0017934.
XX
PA (GETH ) GENENTECH INC.
XX
PI Caras IW;
XX
DR WPI; 1995-035649/05.
DR P-PSDB; AAR66683.
XX
PT Liposome(s) for targetting particular cells contg. fusion protein
PT - of glyco:phosphatidyl:inositol anchor and heterologous
PT targetting protein, e.g. for delivering toxins to infected or
PT cancer cells.
XX
PS Disclosure; Fig. 1a-1f; 36pp; English.
XX
CC A probe (given in AAQ79865) based on the N-terminal sequence of human
CC decay accelerating factor (DAF) was used to screen a HeLa cell
CC lambda cDNA library. Isolated clones encoding membrane-bound DAF
CC (mDAF) were obtained, and the full sequence of mDAF cDNA was
CC determined (AAQ79863). The GPI signal domain of mDAF may be fused to
CC a heterologous protein and targeted to cell membrane surfaces.
XX
SQ Sequence 2115 BP; 675 A; 419 C; 446 G; 575 T; 0 other;

Query Match 75.3%; Score 1582; DB 16; Length 2115;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
Db     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
Db     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
Db     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
Db     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
Db     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
Db     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
Db     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
Db     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
Db     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
Db    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
Db    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
Db    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
Db    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260

Qy    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
Db    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
Db    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380

Qy    1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
Db    1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy    1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
Db    1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy    1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
Db    1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy    1561 CCACTTATAAAGGAAATAAAAA 1582
Db    1561 CCACTTATAAAGGAAATAAAAA 1582
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RESULT 7
AAN91043
ID   AAN91043 standard; DNA; 2115 BP.
XX
AC   AAN91043;
XX
DT   04-JUL-1990  (first entry)
XX
DE   Decay accelerating factor (DAF) of clones lambda 33 and lambda 47.
XX
KW   DAF; allograft rejection; affinity purification;
KW   autoimmune disease; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..2015
FT                   /*tag= a
FT   mat_peptide     198..1208
FT                   /*tag= b
FT   misc_signal     1146
FT                   /*tag= c
FT                   label= mRNA splice site.
XX
PN   WO8901041-A.
XX
PD   09-FEB-1989.
XX
PF   03-AUG-1988;   88WO-US02648.
XX
PR   06-AUG-1987;   87US-0083757.
XX
PA   (GETH ) GENETECH INC.
XX
PI   Caras I;
XX
DR   WPI; 1989-061177/08.
DR   P-PSDB; AAP94773.
XX
PT   Fusion polypeptide for targeting protein to cell membrane -
PT   comprisesphospholipid anchor domain with heterologous
PT   polypeptide.
XX
PS   Disclosure; ; 61pp; English.
XX
CC   Recombinant DAF's are useful in treatment of inflamatory or cell lytic
CC   autoimmune diseases and allograft rejection. Useful in diagnostic
CC   compositions or in affinity purification.
XX
SQ   Sequence 2115 BP; 682 A; 419 C; 446 G; 568 T; 0 other;

  Query Match             72.8%;  Score 1530;  DB 10;  Length 2115;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1530;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260

Qy    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
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Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGA 1530
          |||||||||||||||||||||||||||||
Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGA 1530
```

RESULT 8
AAN70047
ID  AAN70047 standard; cDNA; 2015 BP.
XX
AC  AAN70047;
XX
DT  03-OCT-2002 (updated)
DT  03-FEB-1991 (first entry)
XX
DE  Encodes human decay acceleration factor variant #1.
XX
KW  Decay acceleration factor; ds.
XX
OS  Homo sapiens.
XX

| FH | Key | Location/Qualifiers |
|---|---|---|
| FT | misc_feature | 1147 |
| FT | | /*tag= a |
| FT | | /label=mRNA splice site |
| FT | mat_peptide | 66..1210 |
| FT | | /*tag= b |
| FT | | /product=decay acceleration factor variant |

XX
PN  EP244267-A.
XX
PD  04-NOV-1987.
XX
PF  01-MAY-1987; 87EP-0303944.
XX
PR  02-MAY-1986; 86US-0859107.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Caras IW;
XX
DR  WPI; 1987-308481/44.
DR  P-PSDB; AAP70048.
XX
PT  New decay accelerating factor variants - obtained with the factor by
PT  using recombinant DNA procedures.
XX
PS  Disclosure; Page 15-17; 20pp; English.
XX
CC  The cDNA sequence is that of clones phage lambda 33 (to the
CC  HindIII site at residue 1) and phage lambda 47 (HindIII to
CC  the 3' end) encoding a variant of DAF. DAF and variants are
CC  useful for treating paraoxysmal nocturnal haemoglobinuria,
CC  or inflammatory or cell lytic autoimmune diseases. They may
CC  be used to ameliorate allograft rejection or autoimmune
CC  diseases. See also AAN70046, AAN70048.
CC  (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ  Sequence 2015 BP; 639 A; 402 C; 427 G; 547 T; 0 other;

Query Match 66.7%; Score 1401; DB 8; Length 2015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260

Qy    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380

Qy    1381 GTCCTGGAATCACATTCTTAG 1401
           |||||||||||||||||||||
Db    1381 GTCCTGGAATCACATTCTTAG 1401
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RESULT 9
AAX87915

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ID   AAX87915 standard; cDNA; 1493 BP.
XX
AC   AAX87915;
XX
DT   22-NOV-1999  (first entry)
XX
DE   Human tumour associated antigen 791Tgp72 cDNA.
XX
KW   791Tgp72; tumour associated antigen; CD55; colorectal cancer;
KW   breast cancer; ovary cancer; osteosarcoma; vaccine; human; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             199..1344
FT                   /*tag= a
XX
PN   WO9943800-A1.
XX
PD   02-SEP-1999.
XX
PF   26-FEB-1999;   99WO-GB00582.
XX
PR   26-FEB-1998;   98GB-0004065.
XX
PA   (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI   Durrant LG,  Spendlove I;
XX
DR   WPI; 1999-540585/45.
DR   P-PSDB; AAY31740.
XX
PT   Cancer vaccine containing CD55 family polypeptide, to induce at
PT   least one of T helper, cytotoxic T cell or natural killer immune
PT   response
XX
PS   Claim 14; Fig 11; P 82pp; English.
XX
CC   This is the nucleotide sequence of cDNA coding for human 791Tgp72
CC   (see AAY31740), a new member of the CD55 family that is over-expressed
CC   on a wide range of solid tumours.  The cDNA was isolated from
CC   osteosarcoma cell line 791T cell cDNA by PCR amplification using
CC   primers (see AAX87916-22) based on an isolated N-terminal peptide of
CC   791Tgp72.  A claimed cancer vaccine comprises a polypeptide of the
CC   CD55 family, including full-length CD55 or 791Tgp72, or an antigen,
CC   polypeptide, fragment or derivative of CD55 or 791Tgp72.  Claimed
CC   cancer vaccines also include nucleic acids encoding CD55 or 791Tgp72
CC   antigen, polypeptide, fragment or derivative.  Claimed methods of
CC   treating a cancer patient involve administering the cancer vaccine.
CC   CD55 and 791Tgp72 have identical amino acid sequences and are
CC   encoded by cDNA which is identical over the entire coding region,
CC   through differences exist in the 5' and 3' non-coding regions and
CC   in the glycosylation pattern of the proteins.  The cancer vaccines
CC   induce at least one of T helper, cytotoxic T cell or natural killer
CC   immune responses, possibly also production of neutralizing
CC   antibodies and complement-mediated lysis.  They are useful for
CC   treating e.g. colorectal, breast or ovarian cancer or osteosarcoma,
CC   where these are associated with overexpression of 791Tgp72.
XX
SQ   Sequence 1493 BP; 401 A; 355 C; 355 G; 382 T; 0 other;
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Query Match 64.5%; Score 1356; DB 20; Length 1493;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197

Qy      65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257

Qy     125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317

Qy     185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377

Qy     245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437

Qy     305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497

Qy     365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557

Qy     425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617

Qy     485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677

Qy     545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737

Qy     605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797

Qy     665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857

Qy     725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917

Qy     785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977
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Qy     845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037

Qy     905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097

Qy     965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157

Qy    1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217

Qy    1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277

Qy    1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337

Qy    1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397

Qy    1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457

Qy    1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
           |||||||||||||||||||||||||||||||||||||
Db    1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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RESULT 10
AAQ99105
ID   AAQ99105 standard; cDNA to mRNA; 2096 BP.
XX
AC   AAQ99105;
XX
DT   20-DEC-1995  (first entry)
XX
DE   Human DAF cDNA.
XX
KW   Chimeric complement inhibitor; C3 inhibitor; transplantation;
KW   transgenic animal; gene therapy; DAF; decay acceleration factor;
KW   ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..1199
FT                   /*tag=  a
FT   sig_peptide     54..155
FT                   /*tag=  b
FT   mat_peptide     156..1196
FT                   /*tag=  c
XX
PN   WO9523856-A1.
XX
PD   08-SEP-1995.
XX
PF   01-MAR-1995;   95WO-US02945.
XX
PR   03-MAR-1994;   94US-0205508.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Fodor WL,  Rollins S,  Squinto SP;
XX
DR   WPI; 1995-320571/41.
XX
PT   Chimeric proteins having both C3 and C5b-9 complement inhibitory
PT   activity - useful for protecting non-human organs against complement
PT   attack, e.g. in transplantation
XX
PS   Disclosure; Page 45-47; 83pp; English.
XX
CC   Chimeric complement inhibitor proteins (CIPs) comprise: a functional
CC   domain (FD) having complement C3 inhibitory activity, e.g. human
CC   mature DAF (encoded by the sequence given in AAQ99105) or MCP
CC   (AAQ99106); and a FD having C5b-9 inhibitory activity, e.g. human
CC   mature CD59 (AAQ99104), non-human primate C5b-9 inhibitors (AAQ99107-11)
CC   or mature HVS-15 inhibitor (AAQ99112).  The CIPs allow safe,
CC   effective xerotransplantation of transgenic animal organs
CC   expressing such proteins into humans.
XX
SQ   Sequence 2096 BP; 671 A; 416 C; 439 G; 570 T; 0 other;

  Query Match             59.1%;  Score 1243;  DB 16;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
           ||||||||||||||||
Db    1381 CATTCTTAGCACACCT 1396
```

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RESULT 11
AAT84471
ID   AAT84471 standard; cDNA to mRNA; 2096 BP.
XX
AC   AAT84471;
XX
DT   17-NOV-1997  (first entry)
XX
DE   Human DAF cDNA.
XX
KW   DAF; decay accelerating factor; human; C3 complement inhibitor;
KW   retrovirus; vector; gene therapy; stem cell; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..1199
FT                   /*tag= a
FT   sig_peptide     54..155
FT                   /*tag= b
FT   mat_peptide     156..1196
FT                   /*tag= c
XX
PN   US5643770-A.
XX
PD   01-JUL-1997.
XX
PF   21-JUL-1994;   94US-0278630.
XX
PR   21-JUL-1994;   94US-0278630.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Mason JM,  Squinto SP;
XX
DR   WPI; 1997-350243/32.
DR   P-PSDB; AAW26317.
XX
PT   Retroviral vector particle expressing complement inhibitor activity
PT   - for transducing cells in body fluids containing complement
XX
PS   Disclosure; Column 41-46; 32pp; English.
XX
CC   This cDNA clone codes for human decay accelerating factor (DAF)
CC   (AAW26317), a protein that has C3 complement inhibitor activity.
CC   Claimed retroviral vector particles express a complement inhibitor
CC   such as DAF, and are thereby protected from inactivation upon
CC   exposure to body fluids containing complement. Also claimed are: (1)
CC   a producer cell producing the vector particle; and (2) a chimeric
CC   retroviral envelope protein (see also AAW26326) with at least part of
CC   the N-terminal receptor-binding domain removed and replaced by a
CC   protein domain having a complement inhibitor activity.  The vector
CC   is used in a claimed method for transducing cells in the presence of
CC   a body fluid containing complement, preferably ex vivo, especially
CC   for gene therapy, e.g. of hereditary or acquired blood disorders by
CC   transduction of haematopoietic stem cells.
XX
SQ   Sequence 2096 BP; 671 A; 416 C; 439 G; 570 T; 0 other;
```

Query Match 59.1%; Score 1243; DB 18; Length 2096;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540
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Qy     553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
           ||||||||||||||||
Db    1381 CATTCTTAGCACACCT 1396
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RESULT 12
AAN70048

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ID   AAN70048 standard; DNA; 2233 BP.
XX
AC   AAN70048;
XX
DT   03-OCT-2002  (updated)
DT   03-FEB-1991  (first entry)
XX
DE   Encodes human decay acceleration factor variant #2.
XX
KW   Decay acceleration factor; sDAF; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     66..1388
FT                   /*tag= a
FT                   /product=sDAF
XX
PN   EP244267-A.
XX
PD   04-NOV-1987.
XX
PF   01-MAY-1987;   87EP-0303944.
XX
PR   02-MAY-1986;   86US-0859107.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1987-308481/44.
DR   P-PSDB; AAP70049.
XX
PT   New decay accelerating factor variants - obtained with the factor by
PT   using recombinant DNA procedures.
XX
PS   Disclosure; Page 18-20; 20pp; English.
XX
CC   The cDNA sequence is that of clones phage lambda 33 (to the
CC   HindIII site at residue 1) and phage lambda 41 (HindIII to
CC   the 3' end) encoding a variant of DAF (sDAF).  DAF and
CC   variants are useful for treating paraoxysmal nocturnal
CC   haemoglobinuria, or inflammatory or cell lytic autoimmune
CC   diseases.  They may be used to ameliorate allograft
CC   rejection or autoimmune diseases.  See also AAN70046, AAN70047.
CC   (Updated on 03-OCT-2002 to add missing OS field.)
XX
SQ   Sequence 2233 BP; 695 A; 455 C; 475 G; 608 T; 0 other;
```

Query Match 54.6%; Score 1147; DB 8; Length 2233;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGG 1147
          |||||||
Db   1141 TATCTGG 1147
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RESULT 13
AAN91044
ID   AAN91044 standard; DNA; 2233 BP.
XX
AC   AAN91044;
XX
DT   04-JUL-1990  (first entry)
XX
DE   Membrane bound decay accelerating factor (sDAF).
XX
KW   DAF; allograft rejection; affinity purification;
KW   autoimmune disease; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1385
FT                   /*tag= a
FT   mat_peptide     168..1385
FT                   /*tag= b
XX
PN   WO8901041-A.
XX
PD   09-FEB-1989.
XX
PF   03-AUG-1988;   88WO-US02648.
XX
PR   06-AUG-1987;   87US-0083757.
XX
PA   (GETH ) GENETECH INC.
XX
PI   Caras I;
XX
DR   WPI; 1989-061177/08.
DR   P-PSDB; AAP94774.
XX
PT   Fusion polypeptide for targeting protein to cell membrane -
PT   comprisesphospholipid anchor domain with heterologous
PT   polypeptide.
XX
PS   Disclosure; ; 61pp; English.
XX
CC   Recombinant DAF's are useful in treatment of inflamatory or cell lytic
CC   autoimmune diseases and allograft rejection. Useful in diagnostic
CC   compositions or in affinity purification.
CC   CDS differs from the mature peptide by sequence encoding the secretory
CC   leader.
XX
SQ   Sequence 2233 BP; 695 A; 455 C; 476 G; 607 T; 0 other;

  Query Match             54.6%;  Score 1147;  DB 10;  Length 2233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
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Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGG 1147
          |||||||
Db   1141 TATCTGG 1147
```

```
RESULT 14
AAQ79864
ID   AAQ79864 standard; cDNA; 2233 BP.
XX
AC   AAQ79864;
XX
DT   23-JUL-1995  (first entry)
XX
DE   Decay accelerating factor cDNA.
XX
KW   Decay accelerating factor; DAF; sDAF; fusion protein; liposome;
KW   cell targeting; glycophosphatidylinositol; GPI; drug delivery; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             66..1388
FT                   /*tag=  a
FT   sig_peptide     66..167
FT                   /*tag=  b
FT   mat_peptide     168..1385
FT                   /*tag=  c
FT                   /product= mature sDAF protein
XX
PN   US5374548-A.
XX
PD   20-DEC-1994.
XX
PF   02-MAY-1986;   86US-0859107.
XX
PR   02-MAY-1986;   86US-0859107.
PR   06-AUG-1987;   87US-0083757.
PR   19-DEC-1991;   91US-0811048.
PR   12-FEB-1993;   93US-0017934.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1995-035649/05.
DR   P-PSDB; AAR66684.
XX
PT   Liposome(s) for targetting particular cells contg. fusion protein
PT    - of glyco:phosphatidyl:inositol anchor and heterologous
PT   targetting protein, e.g. for delivering toxins to infected or
PT   cancer cells.
XX
PS   Disclosure; Fig. 2a-2g; 36pp; English.
XX
CC   A probe (given in AAQ79865) based on the N-terminal sequence of human
CC   decay accelerating factor (DAF) was used to screen a HeLa cell
CC   lambda cDNA library.  Isolated clones encoding soluble DAF
CC   (sDAF) were obtained; the full sequence of sDAF cDNA is given in
CC   AAQ79864 and the deduced protein sequence in AAR66684.
XX
SQ   Sequence 2233 BP; 695 A; 456 C; 474 G; 608 T; 0 other;
```

```
  Query Match             54.6%;  Score 1147;  DB 16;  Length 2233;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGG 1147
          |||||||
Db   1141 TATCTGG 1147
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RESULT 15
AAV08935
ID   AAV08935 standard; cDNA to mRNA; 1146 BP.
XX
AC   AAV08935;
XX
DT   01-MAR-1999  (first entry)
XX
DE   DAF protein coding sequence.
XX
KW   DAF; decay accelerating factor; human; compliment protein; gene therapy;
KW   viral vector; ds.
XX
OS   Homo sapiens.
XX
PN   JP10313865-A.
XX
PD   02-DEC-1998.
XX
PF   15-MAY-1997;   97JP-0125965.
XX
PR   15-MAY-1997;   97JP-0125965.
XX
PA   (DINA-) DINABEKKU KENKYUSHO KK.
XX
DR   WPI; 1999-074147/07.
DR   P-PSDB; AAW73505.
XX
PT   Vector having complement controlling factor - useful for gene
PT   therapy
XX
PS   Example 3; Page 8-9; 15pp; Japanese.
XX
CC   This sequence encodes the human decay accelerating factor (DAF) protein.
CC   DAF can be used in the viral vector of the invention. The viral vector
CC   contains a factor controlling the function of a human complement protein,
CC   particularly a membrane combining type protein. The viral vector, which
CC   is stable in situ, is useful for gene therapy.
XX
SQ   Sequence 1146 BP; 325 A; 277 C; 260 G; 284 T; 0 other;

  Query Match            54.5%;  Score 1146;  DB 20;  Length 1146;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1146;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      66 ATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGG 125
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 ATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGG 60

Qy     126 CTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCA 185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCA 120

Qy     186 GATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTA 245
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTA 180

Qy     246 ATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATC 305
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 ATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATC 240

Qy     306 TGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTG 365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 TGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTG 300

Qy     366 CCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCA 425
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCA 360

Qy     426 GTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCA 485
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCA 420

Qy     486 CCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAG 545
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAG 480

Qy     546 AAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATA 605
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATA 540

Qy     606 TTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACT 665
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACT 600

Qy     666 TCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGC 725
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGC 660

Qy     726 AGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGT 785
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGT 720

Qy     786 GACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATT 845
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATT 780

Qy     846 GGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCA 905
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCA 840

Qy     906 CCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACC 965
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACC 900

Qy     966 ACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACC 1025
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACC 960

Qy    1026 ACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTT 1085
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTT 1020

Qy    1086 CATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCT 1145
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCT 1080

Qy    1146 GGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTG 1205
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTG 1140

Qy    1206 ACTTAG 1211
          ||||||
Db    1141 ACTTAG 1146


Search completed: February 24, 2003, 02:48:34
Job time : 476.373 secs
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 01:55:27 ; Search time 5439.47 Seconds
(without alignments)
11246.328 Million cell updates/sec

Title: US-09-623-035-1
Perfect score: 2102
Sequence: 1 ccgctgggcgtagctgcgac.....aaatgatcccatttttggt 2102

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
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19: em_mu:*
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21: em_or:*
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33: em_htg_mus:*
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35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| | 1 | 2102 | 100.0 | 2102 | 6 | AX018846 | AX018846 Sequence |
| | 2 | 2102 | 100.0 | 2102 | 6 | AX333057 | AX333057 Sequence |
| | 3 | 2102 | 100.0 | 2102 | 9 | HUMDAFB | M31516 Human decay |
| | 4 | 1968 | 93.6 | 2263 | 6 | AX202076 | AX202076 Sequence |
| | 5 | 1582 | 75.3 | 2115 | 6 | I05091 | I05091 Sequence 2 |
| | 6 | 1582 | 75.3 | 2115 | 6 | I09215 | I09215 Sequence 1 |
| | 7 | 1356 | 64.5 | 1493 | 6 | AX018850 | AX018850 Sequence |
| | 8 | 1314 | 62.5 | 1357 | 9 | BC001288 | BC001288 Homo sapi |
| | 9 | 1243 | 59.1 | 2096 | 6 | I41330 | I41330 Sequence 1 |
| | 10 | 1243 | 59.1 | 2096 | 6 | I49078 | I49078 Sequence 1 |
| | 11 | 1243 | 59.1 | 2096 | 6 | I50941 | I50941 Sequence 10 |
| | 12 | 1175 | 55.9 | 2017 | 9 | HUMDAF | M15799 Human compl |
| | 13 | 1147 | 54.6 | 2220 | 9 | HUMDAFA | M30142 Human decay |
| | 14 | 1147 | 54.6 | 2233 | 6 | I09216 | I09216 Sequence 3 |
| | 15 | 1097 | 52.2 | 2237 | 6 | A65264 | A65264 Sequence 1 |
| | 16 | 1096 | 52.1 | 2233 | 6 | I05094 | I05094 Sequence 5 |
| | 17 | 1066 | 50.7 | 1313 | 9 | HSU88576 | U88576 Human decay |
| | 18 | 1060 | 50.4 | 2162 | 9 | AY055758 | AY055758 Homo sapi |
| | 19 | 1027 | 48.9 | 1735 | 9 | AF052110 | AF052110 Homo sapi |
| | 20 | 970 | 46.1 | 1848 | 6 | AX134168 | AX134168 Sequence |
| | 21 | 970 | 46.1 | 1878 | 6 | AR031710 | AR031710 Sequence |
| | 22 | 957 | 45.5 | 1077 | 6 | AX014893 | AX014893 Sequence |
| | 23 | 957 | 45.5 | 141124 | 9 | AL391597 | AL391597 Human DNA |
| | 24 | 816 | 38.8 | 969 | 6 | AR066586 | AR066586 Sequence |
| | 25 | 816 | 38.8 | 969 | 6 | I70309 | I70309 Sequence 12 |
| | 26 | 810 | 38.5 | 167359 | 2 | AC031978 | AC031978 Homo sapi |
| | 27 | 707 | 33.6 | 860 | 6 | AR066589 | AR066589 Sequence |
| | 28 | 707 | 33.6 | 860 | 6 | I70312 | I70312 Sequence 19 |
| | 29 | 684 | 32.5 | 1266 | 9 | AF149760 | AF149760 Pan trogl |
| | 30 | 677 | 32.2 | 925 | 9 | AY055759 | AY055759 Homo sapi |
| | 31 | 594 | 28.3 | 1515 | 9 | AY055760 | AY055760 Homo sapi |
| | 32 | 539 | 25.6 | 1266 | 9 | AF149759 | AF149759 Gorilla g |
| | 33 | 520 | 24.7 | 559 | 6 | AX018849 | AX018849 Sequence |
| | 34 | 467 | 22.2 | 1864 | 9 | AY055757 | AY055757 Homo sapi |
| | 35 | 434 | 20.6 | 1140 | 9 | AF149761 | AF149761 Pan trogl |
| | 36 | 401 | 19.1 | 142672 | 2 | AL355527 | AL355527 Homo sapi |
| | 37 | 393 | 18.7 | 586 | 6 | AX018848 | AX018848 Sequence |
| | 38 | 354 | 16.8 | 400 | 11 | G11240 | G11240 human STS S |
| c | 39 | 279 | 13.3 | 586 | 6 | AX335240 | AX335240 Sequence |
| c | 40 | 240 | 11.4 | 479 | 6 | AX261635 | AX261635 Sequence |
| | 41 | 238 | 11.3 | 1245 | 9 | S67775 | S67775 decay-accel |
| c | 42 | 221 | 10.5 | 224 | 6 | AX341675 | AX341675 Sequence |
| | 43 | 192 | 9.1 | 130935 | 9 | AL596218 | AL596218 Human DNA |
| | 44 | 192 | 9.1 | 150933 | 2 | AC010829 | AC010829 Homo sapi |
| c | 45 | 186 | 8.8 | 375 | 11 | G28412 | G28412 human STS S |
| | 46 | 169 | 8.0 | 2003 | 9 | HUMDAFC1 | M64356 Human decay |
| | 47 | 115 | 5.5 | 747 | 6 | AR016516 | AR016516 Sequence |
| | 48 | 115 | 5.5 | 747 | 6 | AR096899 | AR096899 Sequence |
| | 49 | 114 | 5.4 | 134 | 6 | AR016512 | AR016512 Sequence |
| c | 50 | 114 | 5.4 | 134 | 6 | AR016513 | AR016513 Sequence |
| | 51 | 114 | 5.4 | 134 | 6 | AR096895 | AR096895 Sequence |
| c | 52 | 114 | 5.4 | 134 | 6 | AR096896 | AR096896 Sequence |
| | 53 | 114 | 5.4 | 300 | 6 | AR016514 | AR016514 Sequence |
| | 54 | 114 | 5.4 | 300 | 6 | AR096897 | AR096897 Sequence |
| | 55 | 114 | 5.4 | 314 | 6 | I64711 | I64711 Sequence 1 |
| | 56 | 114 | 5.4 | 314 | 6 | I64712 | I64712 Sequence 3 |
| | 57 | 114 | 5.4 | 314 | 6 | I64713 | I64713 Sequence 4 |
| | 58 | 114 | 5.4 | 786 | 6 | AR016518 | AR016518 Sequence |
| | 59 | 114 | 5.4 | 786 | 6 | AR096901 | AR096901 Sequence |
| | 60 | 109 | 5.2 | 674 | 9 | AB003312 | AB003312 Homo sapi |
| | 61 | 109 | 5.2 | 674 | 9 | AB003313 | AB003313 Pan trogl |
| | 62 | 109 | 5.2 | 674 | 9 | AB003314 | AB003314 Pongo pyg |
| | 63 | 107 | 5.1 | 989 | 6 | I64714 | I64714 Sequence 5 |
| | 64 | 103 | 4.9 | 546 | 9 | HUMDAFC5 | M64652 Human decay |
| | 65 | 84 | 4.0 | 662 | 9 | AB003316 | AB003316 Hylobates |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 66 | 84 | 4.0 | 662 | 9 | AB003317 |
| | 67 | 76 | 3.6 | 1250 | 9 | AF149762 |
| | 68 | 76 | 3.6 | 1250 | 9 | AF149763 |
| c | 69 | 72 | 3.4 | 209 | 11 | G22350 |
| | 70 | 68 | 3.2 | 883 | 9 | S51407 |
| | 71 | 68 | 3.2 | 1034 | 9 | AF149766 |
| | 72 | 68 | 3.2 | 1055 | 9 | AF149765 |
| | 73 | 68 | 3.2 | 1250 | 9 | AF149764 |
| | 74 | 68 | 3.2 | 1250 | 9 | AF149767 |
| | 75 | 46 | 2.2 | 848 | 9 | AB003318 |
| c | 76 | 44 | 2.1 | 44 | 6 | I41346 |
| c | 77 | 44 | 2.1 | 44 | 6 | I49094 |
| | 78 | 43 | 2.0 | 761 | 9 | AB003315 |
| | 79 | 39 | 1.9 | 39 | 6 | I41345 |
| | 80 | 39 | 1.9 | 39 | 6 | I49093 |
| | 81 | 34 | 1.6 | 35 | 6 | AX134149 |
| | 82 | 32 | 1.5 | 746 | 9 | AB003319 |
| | 83 | 32 | 1.5 | 1438 | 4 | AF228060 |
| | 84 | 32 | 1.5 | 1546 | 4 | AF228059 |
| | 85 | 32 | 1.5 | 1637 | 6 | AX014811 |
| | 86 | 32 | 1.5 | 1954 | 4 | AF228061 |
| | 87 | 31 | 1.5 | 40 | 6 | I41347 |
| | 88 | 31 | 1.5 | 40 | 6 | I49095 |
| | 89 | 31 | 1.5 | 64 | 9 | S72858 |
| c | 90 | 30 | 1.4 | 33 | 6 | AX134148 |
| | 91 | 30 | 1.4 | 40 | 9 | S70688 |
| c | 92 | 29 | 1.4 | 34 | 6 | I41348 |
| c | 93 | 29 | 1.4 | 34 | 6 | I49096 |
| | 94 | 27 | 1.3 | 2854 | 10 | AB032395 |
| | 95 | 27 | 1.3 | 150381 | 8 | AP003794 |
| | 96 | 27 | 1.3 | 153666 | 8 | AP003287 |
| | 97 | 26 | 1.2 | 33 | 6 | AR066582 |
| | 98 | 26 | 1.2 | 33 | 6 | I70305 |
| | 99 | 25 | 1.2 | 39 | 6 | AR066577 |
| | 100 | 25 | 1.2 | 39 | 6 | I70300 |
| c | 101 | 24 | 1.1 | 45 | 6 | AR066578 |
| c | 102 | 24 | 1.1 | 45 | 6 | I70301 |
| c | 103 | 24 | 1.1 | 106 | 6 | AX134167 |
| | 104 | 24 | 1.1 | 978 | 6 | AX014812 |
| | 105 | 24 | 1.1 | 4812 | 2 | AC018247 |
| c | 106 | 24 | 1.1 | 149198 | 9 | AC007034 |
| | 107 | 24 | 1.1 | 168725 | 2 | AC115886 |
| c | 108 | 24 | 1.1 | 171334 | 3 | AC007477 |
| c | 109 | 24 | 1.1 | 196516 | 3 | AC013450 |
| | 110 | 24 | 1.1 | 197792 | 2 | AC021060 |
| | 111 | 24 | 1.1 | 253305 | 3 | PFMAL3P7 |
| | 112 | 24 | 1.1 | 282071 | 3 | AE003786 |
| c | 113 | 24 | 1.1 | 310779 | 2 | AC005140 |
| c | 114 | 23 | 1.1 | 39 | 6 | AX134164 |
| | 115 | 23 | 1.1 | 13165 | 2 | AC017991 |
| c | 116 | 23 | 1.1 | 24175 | 2 | AC115594 |
| | 117 | 23 | 1.1 | 46943 | 9 | AF165141 |
| | 118 | 23 | 1.1 | 80654 | 3 | AC114394 |
| c | 119 | 23 | 1.1 | 95419 | 2 | OSIG00051 |
| | 120 | 23 | 1.1 | 107600 | 9 | AC084697 |
| | 121 | 23 | 1.1 | 116374 | 2 | AC012834 |
| | 122 | 23 | 1.1 | 126829 | 8 | OSJN00032 |
| c | 123 | 23 | 1.1 | 131134 | 2 | AC120828 |
| | 124 | 23 | 1.1 | 133461 | 2 | AC025968 |
| | 125 | 23 | 1.1 | 145588 | 9 | AC010000 |
| | 126 | 23 | 1.1 | 145819 | 2 | AC090255 |
| | 127 | 23 | 1.1 | 149337 | 2 | AC115141 |
| | 128 | 23 | 1.1 | 155410 | 2 | AC112332 |
| | 129 | 23 | 1.1 | 162258 | 9 | AC105748 |
| | 130 | 23 | 1.1 | 168293 | 2 | AC027174 |
| | 131 | 23 | 1.1 | 170394 | 2 | AC024371 |
| c | 132 | 23 | 1.1 | 170465 | 3 | AC091128 |
| | 133 | 23 | 1.1 | 171942 | 2 | AC021715 |
| c | 134 | 23 | 1.1 | 173513 | 2 | AC126681 |
| c | 135 | 23 | 1.1 | 175481 | 3 | AC010007 |
| c | 136 | 23 | 1.1 | 175948 | 2 | AC019192 |
| c | 137 | 23 | 1.1 | 177476 | 2 | AC103159 |
| c | 138 | 23 | 1.1 | 181905 | 9 | CNS01RIB |

AB003317 Hylobates
AF149762 Papio ham
AF149763 Macaca mu
G22350 human STS W
S51407 decay accel
AF149766 Erythroce
AF149765 Erythroce
AF149764 Erythroce
AF149767 Erythroce
AB003318 Ateles ge
I41346 Sequence 17
I49094 Sequence 17
AB003315 Macaca fu
I41345 Sequence 16
I49093 Sequence 16
AX134149 Sequence
AB003319 Cebus ape
AF228060 Sus scrof
AF228059 Sus scrof
AX014811 Sequence
AF228061 Sus scrof
I41347 Sequence 18
I49095 Sequence 18
S72858 DAF (Dr(a-)
AX134148 Sequence
S70688 decay-accel
I41348 Sequence 19
I49096 Sequence 19
AB032395 Rattus no
AP003794 Oryza sat
AP003287 Oryza sat
AR066582 Sequence
I70305 Sequence 8
AR066577 Sequence
I70300 Sequence 3
AR066578 Sequence
I70301 Sequence 4
AX134167 Sequence
AX014812 Sequence
AC018247 Drosophil
AC007034 Homo sapi
AC115886 Mus muscu
AC007477 Drosophil
AC013450 Drosophil
AC021060 Mus muscu
AL034559 Plasmodiu
AE003786 Drosophil
AC005140 Plasmodiu
AX134164 Sequence
AC017991 Drosophil
AC115594 Dictyoste
AF165141 Homo sapi
AC114394 Drosophil
AL732356 Oryza sat
AC084697 Homo sapi
AC012834 Drosophil
AL606619 Oryza sat
AC120828 Rattus no
AC025968 Homo sapi
AC010000 Homo sapi
AC090255 Homo sapi
AC115141 Rattus no
AC112332 Rattus no
AC105748 Homo sapi
AC027174 Homo sapi
AC024371 Homo sapi
AC091128 Drosophil
AC021715 Homo sapi
AC126681 Mus muscu
AC010007 Drosophil
AC019192 Homo sapi
AC103159 Rattus no
AL163052 Human chr

| | | | | | | |
|---|---|---|---|---|---|---|
| | 139 | 23 | 1.1 | 183157 | 2 | AC128323 |
| | 140 | 23 | 1.1 | 189082 | 9 | AL731537 |
| c | 141 | 23 | 1.1 | 190096 | 2 | AC125311 |
| c | 142 | 23 | 1.1 | 197171 | 2 | AC095245 |
| | 143 | 23 | 1.1 | 206872 | 9 | AC104302 |
| | 144 | 23 | 1.1 | 210979 | 2 | AC023055 |
| c | 145 | 23 | 1.1 | 222664 | 2 | AC125056 |
| | 146 | 23 | 1.1 | 268369 | 3 | AC005847 |
| c | 147 | 23 | 1.1 | 300412 | 3 | AE003471 |
| | 148 | 23 | 1.1 | 320565 | 3 | AE003844 |
| c | 149 | 22 | 1.0 | 31 | 6 | AR066583 |
| c | 150 | 22 | 1.0 | 31 | 6 | I70306 |
| c | 151 | 22 | 1.0 | 47 | 6 | I41342 |
| c | 152 | 22 | 1.0 | 47 | 6 | I49090 |
| c | 153 | 22 | 1.0 | 192 | 11 | G38787 |
| c | 154 | 22 | 1.0 | 507 | 3 | AF461314 |
| c | 155 | 22 | 1.0 | 1096 | 3 | AF140044 |
| c | 156 | 22 | 1.0 | 1308 | 8 | OSMYB1308 |
| c | 157 | 22 | 1.0 | 1497 | 3 | DME011672 |
| c | 158 | 22 | 1.0 | 1951 | 3 | AY070499 |
| c | 159 | 22 | 1.0 | 1968 | 10 | MMU46463 |
| c | 160 | 22 | 1.0 | 2190 | 6 | AR174768 |
| c | 161 | 22 | 1.0 | 2426 | 2 | AC020448 |
| c | 162 | 22 | 1.0 | 2426 | 3 | PFU53326 |
| | 163 | 22 | 1.0 | 2459 | 3 | AF205581 |
| c | 164 | 22 | 1.0 | 4887 | 3 | AB010299 |
| | 165 | 22 | 1.0 | 6112 | 6 | AX345564 |
| c | 166 | 22 | 1.0 | 6112 | 6 | AX345565 |
| c | 167 | 22 | 1.0 | 7546 | 3 | DRORAC |
| c | 168 | 22 | 1.0 | 12029 | 3 | AE001399 |
| c | 169 | 22 | 1.0 | 12179 | 5 | D38621 |
| c | 170 | 22 | 1.0 | 20163 | 2 | AC017907 |
| | 171 | 22 | 1.0 | 24833 | 9 | AP001973 |
| c | 172 | 22 | 1.0 | 27302 | 2 | AC020017 |
| | 173 | 22 | 1.0 | 59498 | 3 | AC004252 |
| c | 174 | 22 | 1.0 | 61107 | 2 | AC017941 |
| c | 175 | 22 | 1.0 | 61170 | 2 | AC068163 |
| c | 176 | 22 | 1.0 | 80518 | 2 | PFMAL13PA |
| c | 177 | 22 | 1.0 | 88206 | 2 | AC108604 |
| c | 178 | 22 | 1.0 | 94736 | 2 | AC098670 |
| | 179 | 22 | 1.0 | 96307 | 2 | AC110856 |
| c | 180 | 22 | 1.0 | 97598 | 2 | AC108238 |
| c | 181 | 22 | 1.0 | 98734 | 2 | PFMAL1P2 |
| c | 182 | 22 | 1.0 | 100834 | 9 | AL160411 |
| | 183 | 22 | 1.0 | 104992 | 2 | AC005504 |
| | 184 | 22 | 1.0 | 109027 | 9 | AC096717 |
| c | 185 | 22 | 1.0 | 111499 | 2 | AC096609 |
| c | 186 | 22 | 1.0 | 113031 | 9 | AL445672 |
| | 187 | 22 | 1.0 | 113880 | 3 | PFMAL3P4 |
| c | 188 | 22 | 1.0 | 113880 | 3 | PFMAL3P4 |
| | 189 | 22 | 1.0 | 116079 | 9 | AL365271 |
| c | 190 | 22 | 1.0 | 119638 | 9 | AC024575 |
| | 191 | 22 | 1.0 | 124039 | 2 | AC019900 |
| c | 192 | 22 | 1.0 | 125933 | 2 | AP000709 |
| | 193 | 22 | 1.0 | 135052 | 5 | AL731859 |
| c | 194 | 22 | 1.0 | 136014 | 2 | AC126531 |
| | 195 | 22 | 1.0 | 138056 | 2 | AC094208 |
| c | 196 | 22 | 1.0 | 140524 | 2 | AC111472 |
| | 197 | 22 | 1.0 | 148833 | 9 | AL159990 |
| | 198 | 22 | 1.0 | 149435 | 2 | AC120686 |
| | 199 | 22 | 1.0 | 149915 | 2 | AC021637 |
| | 200 | 22 | 1.0 | 151460 | 9 | AC099816 |
| | 201 | 22 | 1.0 | 153381 | 2 | AP001990 |
| | 202 | 22 | 1.0 | 154335 | 3 | AC008334 |
| | 203 | 22 | 1.0 | 154413 | 2 | AC007862 |
| c | 204 | 22 | 1.0 | 156667 | 9 | AL136094 |
| | 205 | 22 | 1.0 | 156754 | 2 | AC008031 |
| c | 206 | 22 | 1.0 | 156897 | 2 | AC018782 |
| | 207 | 22 | 1.0 | 157308 | 3 | AC022344 |
| c | 208 | 22 | 1.0 | 157657 | 2 | AC074243 |
| c | 209 | 22 | 1.0 | 158174 | 2 | AC123065 |
| c | 210 | 22 | 1.0 | 158548 | 3 | PFMAL3P2 |
| c | 211 | 22 | 1.0 | 159867 | 2 | AC115466 |

AC128323 Rattus no
AL731537 Human DNA
AC125311 Mus muscu
AC095245 Rattus no
AC104302 Homo sapi
AC023055 Homo sapi
AC125056 Mus muscu
AC005847 Drosophil
AE003471 Drosophil
AE003844 Drosophil
AR066583 Sequence
I70306 Sequence 9
I41342 Sequence 13
I49090 Sequence 13
G38787 C12M60 Plas
AF461314 Drosophil
AF140044 Dictyoste
Y11352 O.sativa mR
AJ011672 Drosophil
AY070499 Drosophil
U46463 Mus musculu
AR174768 Sequence
AC020448 Drosophil
U53326 Plasmodium
AF205581 Plasmodiu
AB010299 Drosophil
AX345564 Sequence
AX345565 Sequence
M81887 Drosophila
AE001399 Plasmodiu
D38621 Xenopus lae
AC017907 Drosophil
AP001973 Homo sapi
AC020017 Drosophil
AC004252 Drosophil
AC017941 Drosophil
AC068163 Homo sapi
AL109815 Plasmodiu
AC108604 Rattus no
AC098670 Rattus no
AC110856 Rattus no
AC108238 Rattus no
AL031745 Plasmodiu
AL160411 Human DNA
AC005504 Plasmodiu
AC096717 Homo sapi
AC096609 Rattus no
AL445672 Human DNA
AL008970 Plasmodiu
AL008970 Plasmodiu
AL365271 Human DNA
AC024575 Homo sapi
AC019900 Drosophil
AP000709 Homo sapi
AL731859 Zebrafish
AC126531 Rattus no
AC094208 Rattus no
AC111472 Rattus no
AL159990 Human DNA
AC120686 Rattus no
AC021637 Homo sapi
AC099816 Homo sapi
AP001990 Homo sapi
AC008334 Drosophil
AC007862 Trypanoso
AL136094 Human DNA
AC008031 Trypanoso
AC018782 Homo sapi
AC022344 Drosophil
AC074243 Homo sapi
AC123065 Mus muscu
AL034558 Plasmodiu
AC115466 Rattus no

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 212 | 22 | 1.0 | 160584 | 2 | AC091655 | AC091655 | Trypanoso |
| c 213 | 22 | 1.0 | 162045 | 2 | AC023488 | AC023488 | Trypanoso |
| c 214 | 22 | 1.0 | 162625 | 9 | AC006083 | AC006083 | Homo sapi |
| 215 | 22 | 1.0 | 167757 | 9 | AC116021 | AC116021 | Homo sapi |
| 216 | 22 | 1.0 | 169546 | 2 | AC004157 | AC004157 | Plasmodiu |
| c 217 | 22 | 1.0 | 169806 | 2 | AC126852 | AC126852 | Rattus no |
| 218 | 22 | 1.0 | 170368 | 9 | AC091982 | AC091982 | Homo sapi |
| c 219 | 22 | 1.0 | 170654 | 9 | AC073901 | AC073901 | Homo sapi |
| 220 | 22 | 1.0 | 171617 | 2 | AC013616 | AC013616 | Homo sapi |
| c 221 | 22 | 1.0 | 172904 | 3 | AC007414 | AC007414 | Drosophil |
| 222 | 22 | 1.0 | 172956 | 2 | AC131370 | AC131370 | Rattus no |
| c 223 | 22 | 1.0 | 174036 | 3 | AC010214 | AC010214 | Drosophil |
| c 224 | 22 | 1.0 | 174539 | 2 | AP001974 | AP001974 | Homo sapi |
| c 225 | 22 | 1.0 | 175556 | 9 | AC093113 | AC093113 | Homo sapi |
| 226 | 22 | 1.0 | 175931 | 9 | HS73E6 | AL163193 | Homo sapi |
| 227 | 22 | 1.0 | 176798 | 2 | AC010944 | AC010944 | Homo sapi |
| 228 | 22 | 1.0 | 176930 | 9 | AL353680 | AL353680 | Human DNA |
| 229 | 22 | 1.0 | 177797 | 2 | AC112512 | AC112512 | Homo sapi |
| 230 | 22 | 1.0 | 178253 | 2 | AC107717 | AC107717 | Mus muscu |
| c 231 | 22 | 1.0 | 178332 | 2 | AC115633 | AC115633 | Mus muscu |
| c 232 | 22 | 1.0 | 178651 | 9 | CNS05TDY | AL358275 | Human chr |
| c 233 | 22 | 1.0 | 182091 | 2 | AC109272 | AC109272 | Mus muscu |
| 234 | 22 | 1.0 | 182147 | 9 | AC062032 | AC062032 | Homo sapi |
| 235 | 22 | 1.0 | 186390 | 3 | AC007852 | AC007852 | Drosophil |
| c 236 | 22 | 1.0 | 186665 | 2 | AC127171 | AC127171 | Mus muscu |
| 237 | 22 | 1.0 | 187784 | 2 | AC116150 | AC116150 | Mus muscu |
| 238 | 22 | 1.0 | 190357 | 2 | AC012259 | AC012259 | Homo sapi |
| c 239 | 22 | 1.0 | 191466 | 3 | AC008348 | AC008348 | Drosophil |
| c 240 | 22 | 1.0 | 191923 | 9 | AC109480 | AC109480 | Homo sapi |
| 241 | 22 | 1.0 | 192318 | 2 | AL845339 | AL845339 | Danio rer |
| c 242 | 22 | 1.0 | 192518 | 2 | AC113513 | AC113513 | Mus muscu |
| 243 | 22 | 1.0 | 193234 | 2 | AC024293 | AC024293 | Homo sapi |
| c 244 | 22 | 1.0 | 193289 | 2 | AC102643 | AC102643 | Mus muscu |
| 245 | 22 | 1.0 | 196859 | 9 | AC096740 | AC096740 | Homo sapi |
| 246 | 22 | 1.0 | 197034 | 2 | AC117154 | AC117154 | Rattus no |
| c 247 | 22 | 1.0 | 199782 | 2 | AC130179 | AC130179 | Rattus no |
| 248 | 22 | 1.0 | 200385 | 2 | AC120347 | AC120347 | Mus muscu |
| c 249 | 22 | 1.0 | 202139 | 2 | AC099588 | AC099588 | Mus muscu |
| 250 | 22 | 1.0 | 204652 | 2 | PFMAL13P6 | AL049183 | Plasmodiu |
| c 251 | 22 | 1.0 | 204652 | 2 | PFMAL13P6 | AL049183 | Plasmodiu |
| 252 | 22 | 1.0 | 205429 | 2 | AC005506 | AC005506 | Plasmodiu |
| c 253 | 22 | 1.0 | 209384 | 2 | AC127313 | AC127313 | Mus muscu |
| c 254 | 22 | 1.0 | 213288 | 2 | AL773558 | AL773558 | Danio rer |
| 255 | 22 | 1.0 | 213294 | 2 | AC099778 | AC099778 | Homo sapi |
| c 256 | 22 | 1.0 | 214216 | 2 | AC026609 | AC026609 | Homo sapi |
| c 257 | 22 | 1.0 | 214527 | 9 | CNS0000J | AL049839 | Human chr |
| 258 | 22 | 1.0 | 216825 | 2 | AC108908 | AC108908 | Mus muscu |
| 259 | 22 | 1.0 | 217668 | 2 | AC020561 | AC020561 | Homo sapi |
| c 260 | 22 | 1.0 | 224641 | 2 | AC102505 | AC102505 | Mus muscu |
| c 261 | 22 | 1.0 | 233428 | 2 | AC011064 | AC011064 | Drosophil |
| 262 | 22 | 1.0 | 234112 | 3 | PFMAL4P2 | AL035475 | Plasmodiu |
| 263 | 22 | 1.0 | 253648 | 3 | AE003638 | AE003638 | Drosophil |
| c 264 | 22 | 1.0 | 258872 | 2 | AC104404 | AC104404 | Rattus no |
| c 265 | 22 | 1.0 | 268147 | 2 | AC116966 | AC116966 | Dictyoste |
| c 266 | 22 | 1.0 | 275390 | 3 | AE003831 | AE003831 | Drosophil |
| c 267 | 22 | 1.0 | 287344 | 3 | AE003816 | AE003816 | Drosophil |
| c 268 | 22 | 1.0 | 288411 | 3 | AE003456 | AE003456 | Drosophil |
| c 269 | 22 | 1.0 | 293431 | 2 | PFMAL13P4 | AL049181 | Plasmodiu |
| 270 | 22 | 1.0 | 302672 | 3 | AE003497 | AE003497 | Drosophil |
| 271 | 22 | 1.0 | 318221 | 2 | PFMAL13P3 | AL049184 | Plasmodiu |
| c 272 | 21 | 1.0 | 21 | 6 | AX018854 | AX018854 | Sequence |
| 273 | 21 | 1.0 | 352 | 4 | CFTETRMIC | AJ000554 | Canis fam |
| c 274 | 21 | 1.0 | 357 | 3 | MTDS93673 | Z93673 | D.sibirica |
| c 275 | 21 | 1.0 | 405 | 3 | CEZ83639 | Z83639 | Chelonus sp |
| c 276 | 21 | 1.0 | 626 | 11 | HUMUT7009 | L29696 | Human STS U |
| c 277 | 21 | 1.0 | 680 | 3 | AF109699 | AF109699 | Chironomu |
| c 278 | 21 | 1.0 | 685 | 3 | AF192171 | AF192171 | Chironomu |
| c 279 | 21 | 1.0 | 685 | 3 | AF192174 | AF192174 | Chironomu |
| c 280 | 21 | 1.0 | 685 | 3 | AF192183 | AF192183 | Chironomu |
| c 281 | 21 | 1.0 | 702 | 3 | AF425727 | AF425727 | Archaeoch |
| c 282 | 21 | 1.0 | 721 | 3 | DROARSDA | M35633 | D.melanogas |
| c 283 | 21 | 1.0 | 731 | 3 | DMARS665 | X06883 | Drosophila |
| c 284 | 21 | 1.0 | 909 | 5 | AF262935 | AF262935 | Gallus ga |
| 285 | 21 | 1.0 | 1217 | 5 | AB040448 | AB040448 | Paralicht |
| c 286 | 21 | 1.0 | 1461 | 3 | AF056205 | AF056205 | Plasmodiu |
| 287 | 21 | 1.0 | 1609 | 4 | S69129 | S69129 | interferon- |
| 288 | 21 | 1.0 | 1611 | 4 | S68997 | S68997 | interferon- |
| 289 | 21 | 1.0 | 1776 | 6 | AX027881 | AX027881 | Sequence |
| 290 | 21 | 1.0 | 1815 | 9 | HSA420897 | AJ420897 | Homo sapi |
| 291 | 21 | 1.0 | 2443 | 3 | DMHETDMDA | X58155 | D.melanogas |
| 292 | 21 | 1.0 | 2599 | 9 | BC028391 | BC028391 | Homo sapi |
| 293 | 21 | 1.0 | 3150 | 5 | AB040449 | AB040449 | Paralicht |
| 294 | 21 | 1.0 | 3400 | 9 | AB040965 | AB040965 | Homo sapi |
| 295 | 21 | 1.0 | 5829 | 6 | AX346628 | AX346628 | Sequence |
| 296 | 21 | 1.0 | 6159 | 6 | AX344828 | AX344828 | Sequence |
| c 297 | 21 | 1.0 | 6159 | 6 | AX344829 | AX344829 | Sequence |
| 298 | 21 | 1.0 | 6301 | 6 | AX344693 | AX344693 | Sequence |
| 299 | 21 | 1.0 | 6583 | 6 | AX281160 | AX281160 | Sequence |
| 300 | 21 | 1.0 | 6782 | 6 | AX345679 | AX345679 | Sequence |
| c 301 | 21 | 1.0 | 7382 | 3 | DROGLDGMCA | M29299 | Drosophila |
| 302 | 21 | 1.0 | 8433 | 2 | AC019910 | AC019910 | Drosophil |
| 303 | 21 | 1.0 | 9547 | 6 | AX346406 | AX346406 | Sequence |
| c 304 | 21 | 1.0 | 10359 | 3 | PFARPI | L11172 | Plasmodium |
| 305 | 21 | 1.0 | 11623 | 1 | AE002066 | AE002066 | Deinococc |
| 306 | 21 | 1.0 | 11674 | 10 | AL731865 | AL731865 | Mouse DNA |
| c 307 | 21 | 1.0 | 12029 | 3 | AE001405 | AE001405 | Plasmodiu |
| c 308 | 21 | 1.0 | 14005 | 3 | AE001409 | AE001409 | Plasmodiu |
| c 309 | 21 | 1.0 | 15356 | 2 | AC013887 | AC013887 | Drosophil |
| c 310 | 21 | 1.0 | 15892 | 3 | AE001419 | AE001419 | Plasmodiu |
| 311 | 21 | 1.0 | 18914 | 2 | AC125462 | AC125462 | Mus muscu |
| 312 | 21 | 1.0 | 24180 | 10 | MMU304861 | AJ304861 | Mus muscu |
| c 313 | 21 | 1.0 | 26603 | 2 | AC112791 | AC112791 | Mus muscu |
| c 314 | 21 | 1.0 | 27178 | 3 | U88175 | U88175 | Caenorhabdi |
| 315 | 21 | 1.0 | 28982 | 2 | AC019836 | AC019836 | Drosophil |
| c 316 | 21 | 1.0 | 30459 | 2 | AC073654 | AC073654 | Homo sapi |
| 317 | 21 | 1.0 | 33917 | 9 | AC004410 | AC004410 | Homo sapi |
| 318 | 21 | 1.0 | 36428 | 9 | AC110000 | AC110000 | Homo sapi |
| c 319 | 21 | 1.0 | 37062 | 3 | AF003136 | AF003136 | Caenorhab |
| 320 | 21 | 1.0 | 37200 | 1 | SCE63 | AL035640 | Streptomy |
| 321 | 21 | 1.0 | 38411 | 9 | AC005257 | AC005257 | Homo sapi |
| 322 | 21 | 1.0 | 38817 | 2 | AC099311 | AC099311 | Homo sapi |
| c 323 | 21 | 1.0 | 40179 | 9 | AC004036 | AC004036 | Homo sapi |
| c 324 | 21 | 1.0 | 41706 | 2 | AC103804 | AC103804 | Homo sapi |
| 325 | 21 | 1.0 | 42584 | 9 | AF215839 | AF215839 | Homo sapi |
| c 326 | 21 | 1.0 | 43128 | 9 | AC011558 | AC011558 | Homo sapi |
| c 327 | 21 | 1.0 | 43152 | 2 | AC109626 | AC109626 | Mus muscu |
| 328 | 21 | 1.0 | 47573 | 3 | AF030694 | AF030694 | Plasmodiu |
| c 329 | 21 | 1.0 | 51180 | 2 | AC020235 | AC020235 | Drosophil |
| c 330 | 21 | 1.0 | 52570 | 2 | AC020259 | AC020259 | Drosophil |
| c 331 | 21 | 1.0 | 55161 | 2 | AC130684 | AC130684 | Homo sapi |
| c 332 | 21 | 1.0 | 55973 | 2 | AC079107 | AC079107 | Homo sapi |
| 333 | 21 | 1.0 | 57109 | 2 | AC060767 | AC060767 | Homo sapi |
| 334 | 21 | 1.0 | 57276 | 2 | AC124271 | AC124271 | Homo sapi |
| 335 | 21 | 1.0 | 57594 | 2 | AC104552 | AC104552 | Mus muscu |
| c 336 | 21 | 1.0 | 57594 | 2 | AC104552 | AC104552 | Mus muscu |
| 337 | 21 | 1.0 | 58912 | 2 | AC122771 | AC122771 | Mus muscu |
| 338 | 21 | 1.0 | 59389 | 2 | AC095557 | AC095557 | Rattus no |
| 339 | 21 | 1.0 | 61145 | 9 | AL139130 | AL139130 | Human DNA |
| c 340 | 21 | 1.0 | 64120 | 9 | AL445646 | AL445646 | Human DNA |
| 341 | 21 | 1.0 | 65140 | 2 | AC091676 | AC091676 | Homo sapi |
| c 342 | 21 | 1.0 | 65140 | 2 | AC091676 | AC091676 | Homo sapi |
| 343 | 21 | 1.0 | 66241 | 2 | AC118831 | AC118831 | Rattus no |
| 344 | 21 | 1.0 | 66446 | 2 | AC099921 | AC099921 | Mus muscu |
| 345 | 21 | 1.0 | 66985 | 2 | AC118620 | AC118620 | Mus muscu |
| c 346 | 21 | 1.0 | 67197 | 9 | AF510423S1 | AF510423 | Homo sapi |
| c 347 | 21 | 1.0 | 69037 | 10 | AC003949 | AC003949 | Mus muscu |
| c 348 | 21 | 1.0 | 70069 | 9 | AC005206 | AC005206 | Homo sapi |
| 349 | 21 | 1.0 | 70184 | 9 | AC012441 | AC012441 | Homo sapi |
| 350 | 21 | 1.0 | 70800 | 2 | AC016337 | AC016337 | Homo sapi |
| c 351 | 21 | 1.0 | 71557 | 2 | AC105083 | AC105083 | Homo sapi |
| 352 | 21 | 1.0 | 73661 | 9 | AC074050 | AC074050 | Homo sapi |
| c 353 | 21 | 1.0 | 74037 | 9 | HS1071N3 | AL031728 | Human DNA |
| 354 | 21 | 1.0 | 74874 | 9 | AC110056 | AC110056 | Homo sapi |
| c 355 | 21 | 1.0 | 74931 | 2 | AC121132 | AC121132 | Mus muscu |
| 356 | 21 | 1.0 | 75270 | 9 | AL591048 | AL591048 | Human DNA |
| 357 | 21 | 1.0 | 75733 | 2 | AC006412 | AC006412 | Homo sapi |

| | | | | | | |
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| c | 358 | 21 | 1.0 | 77820 | 2 | AC127660 |
| c | 359 | 21 | 1.0 | 81896 | 9 | AP001614 |
| | 360 | 21 | 1.0 | 82101 | 9 | AC005694 |
| | 361 | 21 | 1.0 | 83110 | 2 | PFMAL13PB |
| c | 362 | 21 | 1.0 | 83110 | 2 | PFMAL13PB |
| | 363 | 21 | 1.0 | 83629 | 2 | AC110485 |
| c | 364 | 21 | 1.0 | 84092 | 9 | AC121156 |
| | 365 | 21 | 1.0 | 85020 | 8 | AB018113 |
| | 366 | 21 | 1.0 | 85757 | 3 | AC001652 |
| c | 367 | 21 | 1.0 | 86005 | 2 | AC021938 |
| | 368 | 21 | 1.0 | 86743 | 9 | AL359873 |
| | 369 | 21 | 1.0 | 86827 | 3 | PFMAL3P5 |
| c | 370 | 21 | 1.0 | 88210 | 9 | AL607062 |
| c | 371 | 21 | 1.0 | 88614 | 2 | AC026865 |
| | 372 | 21 | 1.0 | 89994 | 10 | AF332860S2 |
| | 373 | 21 | 1.0 | 90310 | 9 | AL442066 |
| | 374 | 21 | 1.0 | 91853 | 9 | AC106810 |
| | 375 | 21 | 1.0 | 93925 | 9 | AC090846 |
| c | 376 | 21 | 1.0 | 94106 | 9 | AC005667 |
| c | 377 | 21 | 1.0 | 95571 | 9 | AL354980 |
| c | 378 | 21 | 1.0 | 96080 | 9 | AC097379 |
| c | 379 | 21 | 1.0 | 97386 | 9 | AC037453 |
| c | 380 | 21 | 1.0 | 97773 | 2 | AC106406 |
| | 381 | 21 | 1.0 | 101589 | 2 | AP003897 |
| | 382 | 21 | 1.0 | 103099 | 2 | AC090080 |
| | 383 | 21 | 1.0 | 103331 | 9 | AC073572 |
| c | 384 | 21 | 1.0 | 103483 | 2 | AC111446 |
| c | 385 | 21 | 1.0 | 105470 | 2 | AC116306 |
| c | 386 | 21 | 1.0 | 106174 | 2 | AC016126 |
| c | 387 | 21 | 1.0 | 107705 | 2 | AC130958 |
| | 388 | 21 | 1.0 | 108937 | 9 | AC098593 |
| c | 389 | 21 | 1.0 | 108952 | 2 | AC096600 |
| c | 390 | 21 | 1.0 | 110000 | 2 | AC013622_2 |
| | 391 | 21 | 1.0 | 110000 | 2 | PFMAL4P1_2 |
| c | 392 | 21 | 1.0 | 110000 | 2 | AC021632_1 |
| c | 393 | 21 | 1.0 | 110000 | 3 | AE001572_3 |
| | 394 | 21 | 1.0 | 110000 | 10 | AF162137_0 |
| | 395 | 21 | 1.0 | 111350 | 9 | AL157814 |
| c | 396 | 21 | 1.0 | 111656 | 2 | AC010449 |
| | 397 | 21 | 1.0 | 112644 | 2 | AC111600 |
| | 398 | 21 | 1.0 | 112813 | 2 | AC102504 |
| | 399 | 21 | 1.0 | 113168 | 9 | HSJ779E11 |
| | 400 | 21 | 1.0 | 114233 | 9 | AP000783 |
| | 401 | 21 | 1.0 | 116696 | 3 | PFMAL3P3 |
| c | 402 | 21 | 1.0 | 117432 | 9 | AC108704 |
| | 403 | 21 | 1.0 | 117954 | 9 | AC002065 |
| | 404 | 21 | 1.0 | 118819 | 9 | AC011491 |
| | 405 | 21 | 1.0 | 119407 | 8 | ATF5K20 |
| c | 406 | 21 | 1.0 | 119460 | 9 | AL590431 |
| | 407 | 21 | 1.0 | 119760 | 9 | AC025458 |
| c | 408 | 21 | 1.0 | 119906 | 9 | AC091937 |
| | 409 | 21 | 1.0 | 120861 | 2 | AC131387 |
| | 410 | 21 | 1.0 | 120953 | 2 | AC102902 |
| c | 411 | 21 | 1.0 | 121460 | 2 | AC027330 |
| | 412 | 21 | 1.0 | 121800 | 9 | AL359924 |
| | 413 | 21 | 1.0 | 121949 | 9 | AL157772 |
| | 414 | 21 | 1.0 | 121995 | 9 | AC122686 |
| | 415 | 21 | 1.0 | 122880 | 9 | AC016711 |
| c | 416 | 21 | 1.0 | 124516 | 9 | AP001615 |
| | 417 | 21 | 1.0 | 126138 | 9 | HSAY18000 |
| c | 418 | 21 | 1.0 | 127197 | 9 | HS965N20 |
| | 419 | 21 | 1.0 | 127329 | 9 | AC091895 |
| | 420 | 21 | 1.0 | 127488 | 2 | AC022095 |
| c | 421 | 21 | 1.0 | 129109 | 9 | AL390239 |
| | 422 | 21 | 1.0 | 129285 | 5 | AC091726 |
| | 423 | 21 | 1.0 | 129457 | 9 | AC087507 |
| c | 424 | 21 | 1.0 | 129644 | 2 | AC073304 |
| | 425 | 21 | 1.0 | 130129 | 2 | AC108083 |
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| c | 427 | 21 | 1.0 | 131300 | 2 | AC116844 |
| c | 428 | 21 | 1.0 | 131320 | 9 | AC106744 |
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AC127660 Rattus no
AP001614 Homo sapi
AC005694 Homo sapi
AL109814 Plasmodiu
AL109814 Plasmodiu
AC110485 Rattus no
AC121156 Homo sapi
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AC021938 Homo sapi
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AL034556 Plasmodiu
AL607062 Human DNA
AC026865 Homo sapi
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AL442066 Human DNA
AC106810 Homo sapi
AC090846 Homo sapi
AC005667 Homo sapi
AL354980 Human DNA
AC097379 Homo sapi
AC037453 Homo sapi
AC106406 Rattus no
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AC090080 Homo sapi
AC073572 Homo sapi
AC111446 Rattus no
AC116306 Dictyoste
AC016126 Homo sapi
AC130958 Rattus no
AC098593 Homo sapi
AC096600 Rattus no
Continuation (3 of
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Continuation (2 of
Continuation (4 of
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AL157814 Human DNA
AC010449 Homo sapi
AC111600 Rattus no
AC102504 Mus muscu
AL121675 Human DNA
AP000783 Homo sapi
Z98547 Plasmodium
AC108704 Homo sapi
AC002065 Homo sapi
AC011491 Homo sapi
AL132960 Arabidops
AL590431 Human DNA
AC025458 Homo sapi
AC091937 Homo sapi
AC131387 Homo sapi
AC102902 Mus muscu
AC027330 Homo sapi
AL359924 Human DNA
AL157772 Human DNA
AC122686 Homo sapi
AC016711 Homo sapi
AP001615 Homo sapi
Y18000 Homo sapien
AL035686 Human DNA
AC091895 Homo sapi
AC022095 Homo sapi
AL390239 Human DNA
AC091726 Gallus ga
AC087507 Homo sapi
AC073304 Homo sapi
AC108083 Homo sapi
AC004089 Homo sapi
AC116844 Mus muscu
AC106744 Homo sapi
AL731573 Human DNA
AC106180 Rattus no

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| | 431 | 21 | 1.0 | 131682 | 9 | AL672277 |
| c | 432 | 21 | 1.0 | 132261 | 2 | AC119528 |
| | 433 | 21 | 1.0 | 132823 | 9 | AL138795 |
| c | 434 | 21 | 1.0 | 133498 | 9 | AC091826 |
| c | 435 | 21 | 1.0 | 134019 | 9 | AC003667 |
| c | 436 | 21 | 1.0 | 134124 | 9 | AL160266 |
| | 437 | 21 | 1.0 | 134623 | 2 | AC126235 |
| c | 438 | 21 | 1.0 | 139011 | 9 | AL138832 |
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| c | 440 | 21 | 1.0 | 139544 | 9 | HSDJ85M6 |
| | 441 | 21 | 1.0 | 139958 | 9 | HUAC002519 |
| c | 442 | 21 | 1.0 | 139990 | 2 | AC095599 |
| | 443 | 21 | 1.0 | 140935 | 9 | AC025173 |
| c | 444 | 21 | 1.0 | 141722 | 2 | AC114363 |
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| | 446 | 21 | 1.0 | 141868 | 2 | AC118918 |
| c | 447 | 21 | 1.0 | 142000 | 9 | AC078813 |
| | 448 | 21 | 1.0 | 142210 | 2 | AC104401 |
| | 449 | 21 | 1.0 | 142756 | 9 | AC005844 |
| | 450 | 21 | 1.0 | 142903 | 2 | AL627254 |
| | 451 | 21 | 1.0 | 143244 | 2 | AC087655 |
| | 452 | 21 | 1.0 | 143618 | 9 | AL137856 |
| c | 453 | 21 | 1.0 | 143845 | 2 | AC104901 |
| | 454 | 21 | 1.0 | 144625 | 2 | AC105735 |
| c | 455 | 21 | 1.0 | 144683 | 9 | AC096554 |
| | 456 | 21 | 1.0 | 145253 | 2 | AC096681 |
| c | 457 | 21 | 1.0 | 145256 | 9 | AL360182 |
| c | 458 | 21 | 1.0 | 145437 | 2 | AC009697 |
| c | 459 | 21 | 1.0 | 145945 | 2 | AC119369 |
| | 460 | 21 | 1.0 | 146549 | 9 | AC087692 |
| c | 461 | 21 | 1.0 | 147525 | 2 | AC098608 |
| | 462 | 21 | 1.0 | 148161 | 2 | AC105742 |
| | 463 | 21 | 1.0 | 148177 | 9 | AC083867 |
| | 464 | 21 | 1.0 | 148416 | 9 | AC002089 |
| | 465 | 21 | 1.0 | 148469 | 2 | AC128226 |
| | 466 | 21 | 1.0 | 148541 | 2 | AC119563 |
| | 467 | 21 | 1.0 | 149656 | 2 | AC015573 |
| c | 468 | 21 | 1.0 | 149684 | 9 | AF127936 |
| | 469 | 21 | 1.0 | 149764 | 9 | AC002076 |
| c | 470 | 21 | 1.0 | 150735 | 9 | AC090687 |
| | 471 | 21 | 1.0 | 151162 | 9 | AC024621 |
| | 472 | 21 | 1.0 | 151432 | 2 | AC102454 |
| | 473 | 21 | 1.0 | 151537 | 2 | AP004751 |
| | 474 | 21 | 1.0 | 151552 | 2 | AC023437 |
| c | 475 | 21 | 1.0 | 151978 | 8 | AP002069 |
| | 476 | 21 | 1.0 | 152304 | 2 | AC023032 |
| c | 477 | 21 | 1.0 | 152755 | 9 | AC099666 |
| c | 478 | 21 | 1.0 | 153098 | 2 | AC130186 |
| c | 479 | 21 | 1.0 | 153206 | 2 | AC114864 |
| c | 480 | 21 | 1.0 | 153234 | 2 | AC024717 |
| | 481 | 21 | 1.0 | 153334 | 2 | AC025676 |
| c | 482 | 21 | 1.0 | 153389 | 2 | AC011695 |
| | 483 | 21 | 1.0 | 153422 | 2 | AC023408 |
| c | 484 | 21 | 1.0 | 153477 | 2 | AC006278 |
| c | 485 | 21 | 1.0 | 153749 | 8 | AP003019 |
| c | 486 | 21 | 1.0 | 153805 | 9 | AC090987 |
| c | 487 | 21 | 1.0 | 153825 | 2 | AC016358 |
| | 488 | 21 | 1.0 | 153958 | 2 | AC125101 |
| c | 489 | 21 | 1.0 | 154443 | 9 | AC087315 |
| | 490 | 21 | 1.0 | 154671 | 2 | AC021680 |
| | 491 | 21 | 1.0 | 156060 | 2 | AC004153 |
| c | 492 | 21 | 1.0 | 156140 | 9 | AC067745 |
| c | 493 | 21 | 1.0 | 156194 | 2 | AC017055 |
| | 494 | 21 | 1.0 | 156231 | 2 | AC121449 |
| c | 495 | 21 | 1.0 | 156949 | 9 | AL161652 |
| | 496 | 21 | 1.0 | 157198 | 9 | AC024082 |
| | 497 | 21 | 1.0 | 157295 | 2 | AC097002 |
| | 498 | 21 | 1.0 | 157444 | 2 | AC104156 |
| c | 499 | 21 | 1.0 | 157478 | 2 | AC015515 |
| c | 500 | 21 | 1.0 | 157546 | 2 | AC109181 |
| c | 501 | 21 | 1.0 | 157728 | 2 | AC097185 |
| | 502 | 21 | 1.0 | 157772 | 9 | AC006212 |
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AL672277 Human DNA
AC119528 Rattus no
AL138795 Human DNA
AC091826 Homo sapi
AC003667 Homo sapi
AL160266 Human DNA
AC126235 Canis fam
AL138832 Human DNA
AL135916 Homo sapi
AL121926 Human DNA
AC002519 Human Chr
AC095599 Rattus no
AC025173 Homo sapi
AC114363 Rattus no
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AC078813 Homo sapi
AC104401 Rattus no
AC005844 Homo sapi
AL627254 Danio rer
AC087655 Homo sapi
AL137856 Human DNA
AC104901 Mus muscu
AC105735 Rattus no
AC096554 Homo sapi
AC096681 Canis fam
AL360182 Human DNA
AC009697 Homo sapi
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AC083867 Homo sapi
AC002089 Homo sapi
AC128226 Rattus no
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AC015573 Homo sapi
AF127936 Homo sapi
AC002076 Homo sapi
AC090687 Homo sapi
AC024621 Homo sapi
AC102454 Mus muscu
AP004751 Oryza sat
AC023437 Homo sapi
AP002069 Oryza sat
AC023032 Homo sapi
AC099666 Homo sapi
AC130186 Atelerix
AC114864 Rattus no
AC024717 Homo sapi
AC025676 Homo sapi
AC011695 Homo sapi
AC023408 Homo sapi
AC006278 Plasmodiu
AP003019 Oryza sat
AC090987 Homo sapi
AC016358 Homo sapi
AC125101 Mus muscu
AC087315 Homo sapi
AC021680 Homo sapi
AC004153 Plasmodiu
AC067745 Homo sapi
AC017055 Homo sapi
AC121449 Rattus no
AL161652 Human DNA
AC024082 Human Chr
AC097002 Rattus no
AC104156 Pan trogl
AC015515 Homo sapi
AC109181 Mus muscu
AC097185 Rattus no
AC006212 Homo sapi
AL669923 Mus muscu

| | | | | | | |
|---|---|---|---|---|---|---|
| | 504 | 21 | 1.0 | 158375 | 2 | AC080039 AC080039 Homo sapi |
| | 505 | 21 | 1.0 | 158714 | 8 | AC082644 AC082644 Oryza sat |
| c | 506 | 21 | 1.0 | 158819 | 2 | AC094716 AC094716 Rattus no |
| c | 507 | 21 | 1.0 | 158838 | 9 | AC009696 AC009696 Homo sapi |
| c | 508 | 21 | 1.0 | 158983 | 2 | AC020598 AC020598 Homo sapi |
| c | 509 | 21 | 1.0 | 159692 | 2 | AC013693 AC013693 Homo sapi |
| c | 510 | 21 | 1.0 | 159698 | 9 | AL591718 AL591718 Human DNA |
| | 511 | 21 | 1.0 | 159698 | 9 | AC027269 AC027269 Homo sapi |
| c | 512 | 21 | 1.0 | 159707 | 2 | AL365403 AL365403 Homo sapi |
| | 513 | 21 | 1.0 | 159765 | 2 | AL359533 AL359533 Mus muscu |
| c | 514 | 21 | 1.0 | 159909 | 2 | AC019352 AC019352 Homo sapi |
| | 515 | 21 | 1.0 | 160186 | 2 | AC027759 AC027759 Homo sapi |
| c | 516 | 21 | 1.0 | 160525 | 2 | AC027074 AC027074 Homo sapi |
| | 517 | 21 | 1.0 | 160551 | 2 | AC126468 AC126468 Homo sapi |
| | 518 | 21 | 1.0 | 160601 | 9 | AC093517 AC093517 Homo sapi |
| c | 519 | 21 | 1.0 | 160686 | 9 | AC118002 AC118002 Homo sapi |
| c | 520 | 21 | 1.0 | 160983 | 2 | AC115911 AC115911 Mus muscu |
| | 521 | 21 | 1.0 | 161492 | 9 | AC007780 AC007780 Homo sapi |
| c | 522 | 21 | 1.0 | 161566 | 2 | AC103703 AC103703 Homo sapi |
| | 523 | 21 | 1.0 | 161933 | 2 | AC125796 AC125796 Homo sapi |
| | 524 | 21 | 1.0 | 161985 | 2 | AC125952 AC125952 Rattus no |
| | 525 | 21 | 1.0 | 162139 | 9 | AC104235 AC104235 Homo sapi |
| c | 526 | 21 | 1.0 | 162143 | 2 | AC097553 AC097553 Rattus no |
| | 527 | 21 | 1.0 | 162355 | 2 | AC127887 AC127887 Rattus no |
| | 528 | 21 | 1.0 | 162367 | 2 | AC098960 AC098960 Rattus no |
| c | 529 | 21 | 1.0 | 162873 | 2 | AC114772 AC114772 Homo sapi |
| c | 530 | 21 | 1.0 | 163311 | 2 | AC025096 AC025096 Homo sapi |
| | 531 | 21 | 1.0 | 163566 | 2 | AC107698 AC107698 Mus muscu |
| c | 532 | 21 | 1.0 | 163566 | 2 | AC107698 AC107698 Mus muscu |
| | 533 | 21 | 1.0 | 163897 | 2 | AC106404 AC106404 Rattus no |
| c | 534 | 21 | 1.0 | 164077 | 2 | AC024398 AC024398 Homo sapi |
| | 535 | 21 | 1.0 | 164154 | 2 | AC095211 AC095211 Rattus no |
| | 536 | 21 | 1.0 | 164399 | 3 | PFMAL3P6 Z98551 Plasmodium |
| | 537 | 21 | 1.0 | 164649 | 2 | AC009193 AC009193 Homo sapi |
| c | 538 | 21 | 1.0 | 164824 | 2 | AC073861 AC073861 Homo sapi |
| c | 539 | 21 | 1.0 | 164907 | 3 | AC007146 AC007146 Drosophil |
| | 540 | 21 | 1.0 | 165210 | 2 | AC101542 AC101542 Mus muscu |
| | 541 | 21 | 1.0 | 165727 | 2 | AC018732 AC018732 Homo sapi |
| c | 542 | 21 | 1.0 | 165865 | 2 | AC079958 AC079958 Mus muscu |
| | 543 | 21 | 1.0 | 165908 | 2 | AC095287 AC095287 Rattus no |
| c | 544 | 21 | 1.0 | 165930 | 9 | AC073951 AC073951 Homo sapi |
| c | 545 | 21 | 1.0 | 166664 | 9 | AL441992 AL441992 Human DNA |
| | 546 | 21 | 1.0 | 166747 | 8 | OSJN00208 AL663005 Oryza sat |
| | 547 | 21 | 1.0 | 166777 | 2 | AC106813 AC106813 Homo sapi |
| c | 548 | 21 | 1.0 | 167007 | 2 | AP003556 AP003556 Homo sapi |
| | 549 | 21 | 1.0 | 167340 | 2 | AC111314 AC111314 Rattus no |
| | 550 | 21 | 1.0 | 167596 | 2 | AC013177 AC013177 Drosophil |
| | 551 | 21 | 1.0 | 167974 | 9 | AL591073 AL591073 Human DNA |
| c | 552 | 21 | 1.0 | 168069 | 9 | AC093520 AC093520 Homo sapi |
| c | 553 | 21 | 1.0 | 168347 | 2 | AC025336 AC025336 Homo sapi |
| c | 554 | 21 | 1.0 | 168368 | 9 | AC008415 AC008415 Homo sapi |
| c | 555 | 21 | 1.0 | 168509 | 2 | AC015570 AC015570 Homo sapi |
| c | 556 | 21 | 1.0 | 168575 | 6 | AX134178 AX134178 Sequence |
| c | 557 | 21 | 1.0 | 168575 | 9 | AY062031 AY062031 Homo sapi |
| c | 558 | 21 | 1.0 | 168659 | 2 | AL359883 AL359883 Homo sapi |
| | 559 | 21 | 1.0 | 168674 | 2 | AC021732 AC021732 Homo sapi |
| | 560 | 21 | 1.0 | 168693 | 9 | AC087468 AC087468 Homo sapi |
| c | 561 | 21 | 1.0 | 168703 | 2 | AC021588 AC021588 Homo sapi |
| c | 562 | 21 | 1.0 | 168729 | 2 | AC087418 AC087418 Homo sapi |
| | 563 | 21 | 1.0 | 168814 | 10 | AL591582 AL591582 Mouse DNA |
| c | 564 | 21 | 1.0 | 169124 | 2 | AP001375 AP001375 Homo sapi |
| | 565 | 21 | 1.0 | 169374 | 2 | AC026050 AC026050 Homo sapi |
| c | 566 | 21 | 1.0 | 169431 | 2 | AC131338 AC131338 Mus muscu |
| c | 567 | 21 | 1.0 | 170156 | 9 | AP003174 AP003174 Homo sapi |
| | 568 | 21 | 1.0 | 170299 | 9 | AC021523 AC021523 Homo sapi |
| | 569 | 21 | 1.0 | 170519 | 2 | AC095390 AC095390 Rattus no |
| | 570 | 21 | 1.0 | 170609 | 9 | AC113132 AC113132 Homo sapi |
| | 571 | 21 | 1.0 | 170801 | 3 | AC095014 AC095014 Drosophil |
| | 572 | 21 | 1.0 | 170801 | 9 | AC107925 AC107925 Homo sapi |
| | 573 | 21 | 1.0 | 170970 | 9 | AL512510 AL512510 Human DNA |
| | 574 | 21 | 1.0 | 171100 | 2 | AC118335 AC118335 Rattus no |
| c | 575 | 21 | 1.0 | 171134 | 3 | AC009198 AC009198 Drosophil |
| | 576 | 21 | 1.0 | 171297 | 2 | AC107261 AC107261 Rattus no |
| c | 577 | 21 | 1.0 | 171519 | 2 | AC096445 AC096445 Rattus no |
| | 578 | 21 | 1.0 | 171557 | 8 | OSJN00177 AL662976 Oryza sat |
| | 579 | 21 | 1.0 | 171660 | 2 | AC017103 AC017103 Homo sapi |
| c | 580 | 21 | 1.0 | 171717 | 2 | AC009266 AC009266 Homo sapi |
| | 581 | 21 | 1.0 | 171721 | 9 | AC022821 AC022821 Homo sapi |
| | 582 | 21 | 1.0 | 172334 | 9 | AC010650 AC010650 Homo sapi |
| c | 583 | 21 | 1.0 | 172543 | 2 | AC128697 AC128697 Mus muscu |
| c | 584 | 21 | 1.0 | 172608 | 2 | AC117591 AC117591 Mus muscu |
| | 585 | 21 | 1.0 | 172737 | 2 | AC119321 AC119321 Rattus no |
| | 586 | 21 | 1.0 | 172823 | 2 | AC018740 AC018740 Homo sapi |
| | 587 | 21 | 1.0 | 172921 | 2 | AP002454 AP002454 Homo sapi |
| c | 588 | 21 | 1.0 | 172966 | 9 | AC106798 AC106798 Homo sapi |
| c | 589 | 21 | 1.0 | 172969 | 2 | AC090574 AC090574 Homo sapi |
| | 590 | 21 | 1.0 | 173109 | 2 | AC091400 AC091400 Pan trogl |
| | 591 | 21 | 1.0 | 173285 | 2 | AC094617 AC094617 Rattus no |
| c | 592 | 21 | 1.0 | 173690 | 10 | AC078790 AC078790 Mus muscu |
| c | 593 | 21 | 1.0 | 173696 | 2 | AC111981 AC111981 Rattus no |
| | 594 | 21 | 1.0 | 173917 | 2 | AC112714 AC112714 Homo sapi |
| c | 595 | 21 | 1.0 | 174074 | 9 | AP003385 AP003385 Homo sapi |
| c | 596 | 21 | 1.0 | 174140 | 9 | AC012379 AC012379 Homo sapi |
| | 597 | 21 | 1.0 | 174552 | 2 | AC092941 AC092941 Homo sapi |
| | 598 | 21 | 1.0 | 175270 | 2 | AC112479 AC112479 Homo sapi |
| c | 599 | 21 | 1.0 | 175317 | 9 | AC104298 AC104298 Homo sapi |
| c | 600 | 21 | 1.0 | 175466 | 9 | AL607077 AL607077 Human DNA |
| | 601 | 21 | 1.0 | 175648 | 3 | AC095013 AC095013 Drosophil |
| c | 602 | 21 | 1.0 | 175762 | 2 | AC009761 AC009761 Homo sapi |
| | 603 | 21 | 1.0 | 175774 | 2 | AL358212 AL358212 Homo sapi |
| | 604 | 21 | 1.0 | 175957 | 2 | AL691501 AL691501 Mus muscu |
| | 605 | 21 | 1.0 | 176007 | 30 | AC026015 Ac026015 Homo sapi |
| | 606 | 21 | 1.0 | 176228 | 2 | AC018658 AC018658 Homo sapi |
| c | 607 | 21 | 1.0 | 176289 | 2 | AC129886 AC129886 Atelerix |
| | 608 | 21 | 1.0 | 176694 | 2 | AC018718 AC018718 Homo sapi |
| c | 609 | 21 | 1.0 | 176813 | 2 | AC114584 AC114584 Mus muscu |
| | 610 | 21 | 1.0 | 177028 | 9 | AC025043 AC025043 Homo sapi |
| c | 611 | 21 | 1.0 | 177056 | 9 | AC091843 AC091843 Homo sapi |
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| c | 613 | 21 | 1.0 | 177127 | 2 | AC026287 AC026287 Homo sapi |
| c | 614 | 21 | 1.0 | 177298 | 2 | AC068751 AC068751 Homo sapi |
| c | 615 | 21 | 1.0 | 177370 | 2 | AC111777 AC111777 Rattus no |
| c | 616 | 21 | 1.0 | 177385 | 2 | AC009434 AC009434 Homo sapi |
| | 617 | 21 | 1.0 | 177419 | 2 | AC096425 AC096425 Rattus no |
| | 618 | 21 | 1.0 | 177830 | 2 | AC095259 AC095259 Rattus no |
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| | 620 | 21 | 1.0 | 178208 | 3 | AC008138 AC008138 Drosophil |
| | 621 | 21 | 1.0 | 178210 | 2 | AC023884 AC023884 Homo sapi |
| c | 622 | 21 | 1.0 | 178273 | 2 | AC005308 AC005308 Plasmodiu |
| | 623 | 21 | 1.0 | 178412 | 10 | AL603864 AL603864 Mouse DNA |
| c | 624 | 21 | 1.0 | 178529 | 2 | AC090907 AC090907 Homo sapi |
| | 625 | 21 | 1.0 | 178607 | 3 | AC010068 AC010068 Drosophil |
| c | 626 | 21 | 1.0 | 178722 | 2 | AC098206 AC098206 Rattus no |
| | 627 | 21 | 1.0 | 178803 | 2 | AC032028 AC032028 Homo sapi |
| c | 628 | 21 | 1.0 | 178876 | 2 | AC019254 AC019254 Homo sapi |
| c | 629 | 21 | 1.0 | 178889 | 2 | AC126923 AC126923 Sus scrof |
| c | 630 | 21 | 1.0 | 178930 | 2 | AC126024 AC126024 Mus muscu |
| c | 631 | 21 | 1.0 | 179024 | 2 | AC112551 AC112551 Rattus no |
| c | 632 | 21 | 1.0 | 179068 | 10 | AL627125 AL627125 Mouse DNA |
| | 633 | 21 | 1.0 | 179206 | 9 | CNS01DS6 AL121656 BAC seque |
| | 634 | 21 | 1.0 | 179343 | 2 | AC121904 AC121904 Mus muscu |
| | 635 | 21 | 1.0 | 179417 | 2 | AC126294 AC126294 Rattus no |
| c | 636 | 21 | 1.0 | 179703 | 2 | AC026331 AC026331 Homo sapi |
| c | 637 | 21 | 1.0 | 179759 | 2 | AC117120 AC117120 Rattus no |
| c | 638 | 21 | 1.0 | 179892 | 3 | AC023691 AC023691 Drosophil |
| c | 639 | 21 | 1.0 | 180132 | 2 | AL831756 AL831756 Mus muscu |
| | 640 | 21 | 1.0 | 180142 | 2 | AC091059 AC091059 Homo sapi |
| | 641 | 21 | 1.0 | 180169 | 2 | AC127372 AC127372 Mus muscu |
| c | 642 | 21 | 1.0 | 180290 | 9 | AC005081 AC005081 Homo sapi |
| c | 643 | 21 | 1.0 | 180397 | 9 | AC007035 AC007035 Homo sapi |
| | 644 | 21 | 1.0 | 180492 | 2 | AC124312 AC124312 Homo sapi |
| c | 645 | 21 | 1.0 | 180662 | 2 | AC116044 AC116044 Papio ham |
| c | 646 | 21 | 1.0 | 180760 | 2 | AC130435 AC130435 Homo sapi |
| | 647 | 21 | 1.0 | 180829 | 2 | AC022508 AC022508 Homo sapi |
| c | 648 | 21 | 1.0 | 180851 | 2 | AC090210 AC090210 Homo sapi |
| | 649 | 21 | 1.0 | 180852 | 2 | AC126765 AC126765 Homo sapi |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 650 | 21 | 1.0 | 181003 | 2 | AC127549 |
| | 651 | 21 | 1.0 | 181191 | 2 | AC101738 |
| c | 652 | 21 | 1.0 | 181211 | 2 | AP001904 |
| | 653 | 21 | 1.0 | 181231 | 2 | AC016259 |
| | 654 | 21 | 1.0 | 181502 | 2 | AC107850 |
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| c | 660 | 21 | 1.0 | 183357 | 9 | AC068759 |
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| c | 662 | 21 | 1.0 | 183865 | 9 | AC009084 |
| | 663 | 21 | 1.0 | 184169 | 2 | AC126654 |
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| c | 666 | 21 | 1.0 | 185273 | 9 | AC073320 |
| c | 667 | 21 | 1.0 | 185290 | 9 | AC112206 |
| c | 668 | 21 | 1.0 | 185370 | 2 | AC116210 |
| c | 669 | 21 | 1.0 | 185736 | 2 | AL356011 |
| | 670 | 21 | 1.0 | 185749 | 2 | AC117370 |
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| | 672 | 21 | 1.0 | 185857 | 2 | AC129281 |
| | 673 | 21 | 1.0 | 186001 | 2 | AC130780 |
| | 674 | 21 | 1.0 | 186034 | 10 | AL672036 |
| | 675 | 21 | 1.0 | 186102 | 2 | AC115802 |
| c | 676 | 21 | 1.0 | 186117 | 9 | AC072046 |
| | 677 | 21 | 1.0 | 186199 | 9 | AC093911 |
| | 678 | 21 | 1.0 | 186227 | 2 | AC121418 |
| | 679 | 21 | 1.0 | 186305 | 9 | AL356098 |
| c | 680 | 21 | 1.0 | 186902 | 9 | AC010863 |
| c | 681 | 21 | 1.0 | 187218 | 2 | AC107495 |
| | 682 | 21 | 1.0 | 187443 | 2 | AC107704 |
| | 683 | 21 | 1.0 | 187769 | 2 | AC120959 |
| c | 684 | 21 | 1.0 | 188331 | 2 | AC112876 |
| c | 685 | 21 | 1.0 | 188364 | 9 | AC007784 |
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| c | 687 | 21 | 1.0 | 188642 | 9 | HS55C20 |
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| | 690 | 21 | 1.0 | 189572 | 9 | AC091199 |
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| c | 692 | 21 | 1.0 | 189991 | 2 | AC109182 |
| c | 693 | 21 | 1.0 | 190289 | 10 | AL732540 |
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| | 695 | 21 | 1.0 | 190550 | 2 | AP001797 |
| c | 696 | 21 | 1.0 | 190822 | 2 | AC051613 |
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| c | 700 | 21 | 1.0 | 191119 | 9 | AC009957 |
| | 701 | 21 | 1.0 | 191170 | 2 | AC012235 |
| | 702 | 21 | 1.0 | 191236 | 9 | AC090519 |
| c | 703 | 21 | 1.0 | 191655 | 2 | AC094460 |
| | 704 | 21 | 1.0 | 191735 | 10 | AL596446 |
| | 705 | 21 | 1.0 | 191879 | 2 | AC106412 |
| | 706 | 21 | 1.0 | 191904 | 9 | AC005699 |
| | 707 | 21 | 1.0 | 192097 | 9 | AC008743 |
| | 708 | 21 | 1.0 | 192252 | 2 | AC108971 |
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| c | 711 | 21 | 1.0 | 193156 | 2 | AC125043 |
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| | 713 | 21 | 1.0 | 193484 | 2 | AC126590 |
| c | 714 | 21 | 1.0 | 193509 | 2 | AC026868 |
| | 715 | 21 | 1.0 | 193513 | 2 | AC074372 |
| c | 716 | 21 | 1.0 | 193530 | 2 | AC102438 |
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| | 718 | 21 | 1.0 | 193659 | 10 | AC122438 |
| | 719 | 21 | 1.0 | 193689 | 2 | AC066603 |
| | 720 | 21 | 1.0 | 193985 | 2 | AC099703 |
| c | 721 | 21 | 1.0 | 194439 | 2 | AC122447 |
| c | 722 | 21 | 1.0 | 194459 | 2 | AC104905 |

AC127549 Mus muscu
AC101738 Mus muscu
AP001904 Homo sapi
AC016259 Homo sapi
AC107850 Mus muscu
AC110171 Mus muscu
AC129881 Papio cyn
AP001357 Homo sapi
AC123137 Rattus no
AC007257 Drosophil
AC068759 Homo sapi
AC100406 Mus muscu
AC009084 Homo sapi
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AC112206 Homo sapi
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AC117370 Homo sapi
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AC129281 Rattus no
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AC121418 Rattus no
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AC010863 Homo sapi
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AC120959 Rattus no
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AC007784 Homo sapi
AC120344 Mus muscu
AL021368 Homo sapi
AC016990 Homo sapi
AC103805 Homo sapi
AC091199 Homo sapi
AC004169 Homo sapi
AC109182 Mus muscu
AL732540 Mouse DNA
AC025062 Homo sapi
AP001797 Homo sapi
AC051613 Mus muscu
AC095148 Rattus no
AC114732 Homo sapi
AC091825 Homo sapi
AC009957 Homo sapi
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AC094460 Rattus no
AL596446 Mouse DNA
AC106412 Rattus no
AC005699 Homo sapi
AC008743 Homo sapi
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AC010262 Homo sapi
AC005284 Homo sapi
AC125043 Mus muscu
AC117452 Homo sapi
AC126590 Rattus no
AC026868 Homo sapi
AC074372 Homo sapi
AC102438 Mus muscu
AC021569 Homo sapi
AC122438 Mus muscu
AC066603 Homo sapi
AC099703 Mus muscu
AC122447 Mus muscu
AC104905 Mus muscu

| | | | | | | |
|---|---|---|---|---|---|---|
| c | 723 | 21 | 1.0 | 195155 | 9 | AC110611 |
| c | 724 | 21 | 1.0 | 195370 | 2 | AL390063 |
| | 725 | 21 | 1.0 | 195995 | 2 | AC079800 |
| c | 726 | 21 | 1.0 | 196067 | 2 | AC102083 |
| | 727 | 21 | 1.0 | 196170 | 2 | AC087527 |
| | 728 | 21 | 1.0 | 196420 | 2 | AC108825 |
| c | 729 | 21 | 1.0 | 196721 | 9 | AC019179 |
| | 730 | 21 | 1.0 | 197019 | 9 | AL157938 |
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| c | 732 | 21 | 1.0 | 197843 | 2 | AC024373 |
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| | 735 | 21 | 1.0 | 198319 | 2 | AC067758 |
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| c | 737 | 21 | 1.0 | 198480 | 2 | AC025077 |
| | 738 | 21 | 1.0 | 198804 | 2 | AC122714 |
| | 739 | 21 | 1.0 | 198842 | 9 | AC087587 |
| c | 740 | 21 | 1.0 | 198926 | 10 | AL683843 |
| c | 741 | 21 | 1.0 | 198957 | 2 | AC131390 |
| c | 742 | 21 | 1.0 | 199706 | 2 | AC097329 |
| c | 743 | 21 | 1.0 | 199725 | 2 | AC100787 |
| c | 744 | 21 | 1.0 | 200278 | 9 | AC092797 |
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| c | 747 | 21 | 1.0 | 201157 | 2 | AC079189 |
| c | 748 | 21 | 1.0 | 201787 | 2 | AC093468 |
| | 749 | 21 | 1.0 | 201850 | 2 | AC069476 |
| c | 750 | 21 | 1.0 | 202760 | 2 | AC021987 |
| c | 751 | 21 | 1.0 | 202879 | 2 | AL772334 |
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| | 753 | 21 | 1.0 | 203437 | 2 | AC125468 |
| c | 754 | 21 | 1.0 | 203484 | 2 | AC010194 |
| | 755 | 21 | 1.0 | 203725 | 10 | AC122823 |
| | 756 | 21 | 1.0 | 205759 | 10 | AL669853 |
| c | 757 | 21 | 1.0 | 206102 | 9 | AC027131 |
| c | 758 | 21 | 1.0 | 207018 | 2 | AC102707 |
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| c | 760 | 21 | 1.0 | 207209 | 10 | AL731783 |
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| c | 763 | 21 | 1.0 | 207725 | 2 | AC103191 |
| | 764 | 21 | 1.0 | 207726 | 2 | AC024953 |
| c | 765 | 21 | 1.0 | 208039 | 2 | AC044807 |
| c | 766 | 21 | 1.0 | 208098 | 2 | AL627251 |
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| c | 768 | 21 | 1.0 | 208430 | 2 | AC027641 |
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| | 770 | 21 | 1.0 | 209651 | 2 | AC117596 |
| | 771 | 21 | 1.0 | 210805 | 2 | AC026333 |
| c | 772 | 21 | 1.0 | 211594 | 2 | AC091564 |
| c | 773 | 21 | 1.0 | 211962 | 9 | AC092117 |
| | 774 | 21 | 1.0 | 213084 | 9 | HSG164F24 |
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| | 776 | 21 | 1.0 | 213552 | 9 | AC010928 |
| c | 777 | 21 | 1.0 | 213573 | 2 | AC123056 |
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| c | 780 | 21 | 1.0 | 215467 | 2 | AC013420 |
| | 781 | 21 | 1.0 | 215786 | 9 | AC022916 |
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| c | 786 | 21 | 1.0 | 219256 | 9 | AP001743 |
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| c | 789 | 21 | 1.0 | 226019 | 2 | AC124242 |
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| c | 791 | 21 | 1.0 | 226946 | 2 | AC107792 |
| c | 792 | 21 | 1.0 | 227184 | 2 | AC009868 |
| | 793 | 21 | 1.0 | 227197 | 2 | AC126179 |
| | 794 | 21 | 1.0 | 227320 | 2 | AC113309 |
| c | 795 | 21 | 1.0 | 227737 | 2 | AC099287 |

AC110611 Homo sapi
AL390063 Homo sapi
AC079800 Homo sapi
AC102083 Mus muscu
AC087527 Homo sapi
AC108825 Mus muscu
AC019179 Homo sapi
AL157938 Human DNA
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AC024373 Homo sapi
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AC117798 Mus muscu
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AC009878 Homo sapi
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AC122714 Homo sapi
AC087587 Homo sapi
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AC100787 Homo sapi
AC092797 Homo sapi
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AC093879 Homo sapi
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AC123877 Mus muscu
AP001743 Homo sapi
AC105642 Rattus no
AC005015 Homo sapi
AC124242 Homo sapi
AC022235 Mus muscu
AC107792 Mus muscu
AC009868 Homo sapi
AC126179 Homo sapi
AC113309 Mus muscu
AC099287 Rattus no

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|---|---|---|---|---|---|---|
| c | 796 | 21 | 1.0 | 228802 | 2 | AC023717 |
| | 797 | 21 | 1.0 | 230839 | 10 | AC068561 |
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| | 799 | 21 | 1.0 | 232239 | 2 | AC118348 |
| c | 800 | 21 | 1.0 | 232613 | 9 | AC008679 |
| c | 801 | 21 | 1.0 | 233775 | 2 | AC129336 |
| c | 802 | 21 | 1.0 | 237550 | 2 | AL845325 |
| c | 803 | 21 | 1.0 | 238544 | 2 | AL732472 |
| | 804 | 21 | 1.0 | 242363 | 2 | AC021443 |
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| | 806 | 21 | 1.0 | 244237 | 3 | AE003632 |
| | 807 | 21 | 1.0 | 245802 | 2 | AC006279 |
| | 808 | 21 | 1.0 | 251187 | 2 | AL359875 |
| | 809 | 21 | 1.0 | 252616 | 2 | AC125542 |
| | 810 | 21 | 1.0 | 254525 | 2 | AC106516 |
| c | 811 | 21 | 1.0 | 257728 | 2 | AC006846 |
| c | 812 | 21 | 1.0 | 260624 | 3 | AE003625 |
| c | 813 | 21 | 1.0 | 265938 | 2 | AC127247 |
| c | 814 | 21 | 1.0 | 267486 | 2 | AC103326 |
| | 815 | 21 | 1.0 | 268147 | 2 | AC116966 |
| c | 816 | 21 | 1.0 | 278772 | 2 | AC067734 |
| c | 817 | 21 | 1.0 | 283816 | 2 | AC124587 |
| | 818 | 21 | 1.0 | 286332 | 2 | AC022105 |
| | 819 | 21 | 1.0 | 294308 | 3 | AE003595 |
| | 820 | 21 | 1.0 | 298028 | 3 | AE003674 |
| c | 821 | 21 | 1.0 | 301051 | 3 | AE003487 |
| | 822 | 21 | 1.0 | 304005 | 2 | AC090655 |
| c | 823 | 21 | 1.0 | 307911 | 3 | AE003635 |
| | 824 | 21 | 1.0 | 310779 | 2 | AC005140 |
| c | 825 | 21 | 1.0 | 318221 | 2 | PFMAL13P3 |
| | 826 | 21 | 1.0 | 318488 | 9 | AC005529 |
| c | 827 | 21 | 1.0 | 321003 | 2 | PFMAL4P3 |
| | 828 | 21 | 1.0 | 321914 | 2 | AC126554 |
| | 829 | 21 | 1.0 | 329752 | 2 | AC096334 |
| c | 830 | 21 | 1.0 | 340000 | 9 | HS21C007 |
| c | 831 | 20 | 1.0 | 30 | 6 | AX018856 |
| | 832 | 20 | 1.0 | 34 | 6 | I41341 |
| | 833 | 20 | 1.0 | 34 | 6 | I49089 |
| c | 834 | 20 | 1.0 | 52 | 6 | AR031713 |
| c | 835 | 20 | 1.0 | 55 | 6 | AR031719 |
| c | 836 | 20 | 1.0 | 58 | 6 | AR031718 |
| | 837 | 20 | 1.0 | 65 | 6 | AX483905 |
| c | 838 | 20 | 1.0 | 73 | 6 | AR031711 |
| c | 839 | 20 | 1.0 | 103 | 6 | AR031714 |
| c | 840 | 20 | 1.0 | 298 | 11 | HUMUT1047 |
| c | 841 | 20 | 1.0 | 360 | 9 | AF400622S8 |
| c | 842 | 20 | 1.0 | 377 | 3 | AY040178 |
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AF292013 Reticulit
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AF292007 Reticulit
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AY028751 Batrachup

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Z48432 S. cerevisi

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ALIGNMENTS

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DEFINITION  Sequence 1 from Patent WO9943800.
ACCESSION   AX018846
VERSION     AX018846.1  GI:10042948
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2102)
  AUTHORS   Durrant,L.G. and Spendlove,I.
  TITLE     Tumor associated antigen 791tgp72
  JOURNAL   Patent: WO 9943800-A 1 02-SEP-1999;
            DURRANT LINDA GILLIAN (GB); SPENDLOVE IAN (GB); CANCER RES CAMPAIGN
            TECH (GB)
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                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
BASE COUNT      661 a    419 c    445 g    577 t
ORIGIN

  Query Match           100.0%;  Score 2102;  DB 6;  Length 2102;
  Best Local Similarity 100.0%;  Pred. No. 0;
  Matches 2102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
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Db   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260

Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
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Db   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
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Db   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380

Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
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Db   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620

Qy   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680

Qy   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740

Qy   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800
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Db   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800

Qy   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860
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Db   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860

Qy   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920

Qy   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980

Qy   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
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Db   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100

Qy   2101 GT 2102
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Db   2101 GT 2102
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RESULT 2
AX333057
LOCUS       AX333057               2102 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 3566 from Patent WO0194629.
ACCESSION   AX333057
VERSION     AX333057.1  GI:18123691
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 3566 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .2102
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                     /db_xref="taxon:9606"
BASE COUNT      661 a    419 c    445 g    577 t
ORIGIN

  Query Match             100.0%;  Score 2102;  DB 6;  Length 2102;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2102;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
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Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
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Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
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Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
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Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
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Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
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Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
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Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
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Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
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Qy   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980
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Qy   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
Db   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
Qy   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
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Qy   2101 GT 2102
Db   2101 GT 2102
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RESULT 3
HUMDAFB
LOCUS       HUMDAFB                2102 bp    mRNA    linear   PRI 02-NOV-1994
DEFINITION  Human decay-accelerating factor mRNA, complete cds.
ACCESSION   M31516
VERSION     M31516.1  GI:181467
KEYWORDS    alternative splicing; decay-accelerating factor; membrane
            glycoprotein.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2102)
  AUTHORS   Caras,I.W., Davitz,M.A., Rhee,L., Weddell,G., Martin,D.W. Jr. and
            Nussenzweig,V.
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  TITLE     Cloning of decay-accelerating factor suggests novel use of splicing
            to generate two proteins
  JOURNAL   Nature 325 (6104), 545-549 (1987)
  MEDLINE   87115845
   PUBMED   2433596
COMMENT     The gene for decay accelerating factor produces two proteins by
            alternative splicing.  The spliced out region is between positions
            1147 and 1148.
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                     /cell_line="HeLa"
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                     /gene="DAF"
     mRNA            <1. .2102
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                     /note="G00-119-088"
     CDS             66. .1211
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                     /protein_id="AAA52169.1"
                     /db_xref="GI:181468"
                     /db_xref="GDB:G00-119-088"
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
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     mat_peptide     168. .1208
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                     /note="G00-119-088"
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                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1575. .1580
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1613. .1618
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    2080. .2085
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_site      2102
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BASE COUNT      661 a    419 c    445 g    577 t
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Query Match 100.0%; Score 2102; DB 9; Length 2102;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
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Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
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Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
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Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
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Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
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Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
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Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
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Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
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Db     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
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Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Qy     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
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Db     961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

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Qy    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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Db    1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

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Db    1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
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Db    1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
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Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
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Db   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380

Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
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Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
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Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620
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Db   1561 CCACTTATAAAGGAAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAA 1620

Qy   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 CCCAATTCAGTCTCTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAA 1680

Qy   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TCTTTGGCTGTAAGGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAA 1740

Qy   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 ACATGCTGGTGAACCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTG 1800

Qy   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 AATCTTCCTTTGTTGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGA 1860

Qy   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CTTAATGTCTTTAAAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATA 1920

Qy   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 TTATTTCTGAATCGAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTT 1980

Qy   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 ATTTATATTTATTTATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGA 2040

Qy   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 AGAAGATATGTGAAGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTG 2100

Qy   2101 GT 2102
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Db   2101 GT 2102
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RESULT 4
AX202076
LOCUS       AX202076               2263 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 6 from Patent WO0153531.
ACCESSION   AX202076
VERSION     AX202076.1  GI:15391861
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 2263)
  AUTHORS   Phippard,D., Vasanthakamur,G., Dotson,S. and Ma,X.J.
  TITLE     Osteoarthritis tissue derived nucleic acids, polypeptides, vectors,
            and cells
  JOURNAL   Patent: WO 0153531-A 6 26-JUL-2001;
            Pharmacia Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .2263
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      706 a    475 c    474 g    607 t      1 others
ORIGIN
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Query Match 93.6%; Score 1968; DB 6; Length 2263;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2088; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy     15 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 74
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 TGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCGTC 220

Qy     75 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    221 GCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTG 280

Qy    135 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 194
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    281 CTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCT 340

Qy    195 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 254
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    341 AATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTAC 400

Qy    255 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    401 AAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAG 460

Qy    315 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    461 GGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGG 520

Qy    375 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    521 CTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACT 580

Qy    435 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    581 GTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTA 640

Qy    495 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 554
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    641 ACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGC 700

Qy    555 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 614
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    701 CCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGT 760

Qy    615 GCAACCAT-CTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 673
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    761 GCAACCATGCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTT 820

Qy    674 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    821 TTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAAT 880

Qy    734 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    881 TTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTA 940

Qy    794 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    941 TGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCA 1000
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Qy    854 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1001 CTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATG 1060

Qy    914 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1061 CAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAA 1120

Qy    974 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1033
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1121 TGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACC 1180

Qy   1034 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1093
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1181 AAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAAC 1240

Qy   1094 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1153
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1241 AACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACAC 1300

Qy   1154 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1213
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Db   1301 GTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCC 1360

Qy   1214 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1273
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Db   1361 AAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACT 1420

Qy   1274 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1333
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Db   1421 TATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGT 1480

Qy   1334 CTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCAC 1393
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1481 CTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCAC 1540

Qy   1394 ATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCC 1453
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Db   1541 ATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAATTGAGAGTGATTCC 1600

Qy   1454 TTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGA 1513
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Db   1601 TTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAATGGGATCACGAGGA 1660

Qy   1514 AAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTTCCACTTATAAAGG 1573
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Qy   1574 AAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCT 1633
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Db   1721 AAATAAAAAATGAAAAACATTATTTGGATATCAAAAGCAAATAAAAACCCAATTCAGTCT 1780

Qy   1634 CTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAA 1693
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1781 CTTCTAAGCAAAATTGCTAAAGAGAGATGAACCACATTATAAAGTAATCTTTGGCTGTAA 1840

Qy   1694 GGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAA 1753
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Db   1841 GGCATTTTCATCTTTCCTTCGGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAA 1900

Qy   1754 CCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGT 1813
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Db   1901 CCAGGGGTGTTGATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTTGT 1960

Qy   1814 TGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTA 1873
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Db   1961 TGCACAAATAGAGTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTA 2020

Qy   1874 AAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATC 1933
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2021 AAAGTATCCAGAGATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATC 2080

Qy   1934 GAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATT 1993
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2081 GAGATGTCCATAGTCAAATTTGTAAATCTTATTCTTTTGTAATATTTATTTATATTTATT 2140

Qy   1994 TATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGA 2053
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Db   2141 TATGACAGTGAACATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGA 2200

Qy   2054 AGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2102
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Db   2201 AGAAAAATGTATTTTTCCTAAATAGAAATAAATGATCCCATTTTTTGGT 2249


RESULT 5
I05091
LOCUS       I05091                2115 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 2 from Patent EP 0244267.
ACCESSION   I05091
VERSION     I05091.1  GI:591251
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2115)
  AUTHORS   Caras,I.W.
  TITLE     Variants of decay accelerating factor (DAF) prepared by recombinant
            DNA technology
  JOURNAL   Patent: EP 0244267-A2 2 04-NOV-1987;
FEATURES             Location/Qualifiers
     source          1. .2115
                     /organism="unknown"
BASE COUNT      675 a    419 c    445 g    576 t
ORIGIN

  Query Match             75.3%;  Score 1582;  DB 6;  Length 2115;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1582;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
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Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
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Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
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Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
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Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
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Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
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Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
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Db   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260

Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380

Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy   1561 CCACTTATAAAGGAAATAAAAA 1582
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Db   1561 CCACTTATAAAGGAAATAAAAA 1582
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RESULT 6
I09215
LOCUS       I09215                  2115 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 1 from Patent WO 8901041.
ACCESSION   I09215
VERSION     I09215.1  GI:588075
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2115)
  AUTHORS   Caras,I.W.
  TITLE     NUCLEIC ACID AND METHODS FOR THE SYNTHESIS OF NOVEL FUSION
            POLYPEPTIDES WITH A PHOSPHOLIPID ANCHOR DOMAIN
  JOURNAL   Patent: WO 8901041-A 1 09-FEB-1989;
FEATURES             Location/Qualifiers
     source          1. .2115
                     /organism="unknown"
BASE COUNT      675 a    419 c    446 g    575 t
ORIGIN

  Query Match           75.3%;  Score 1582;  DB 6;  Length 2115;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1582;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
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Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
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Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
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Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
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Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
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Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
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Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
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Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
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Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
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Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
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Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
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Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
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Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
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Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
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Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
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Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200

Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
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Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320
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Db   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGG 1320

Qy   1321 ATGCTTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCA 1380
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Qy   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440
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Db   1381 GTCCTGGAATCACATTCTTAGCACACCTACACCTCTTGAAAATAGAACAACTTGCAGAAT 1440

Qy   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500
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Db   1441 TGAGAGTGATTCCTTTCCTAAAAGTGTAAGAAAGCATAGAGATTTGTTCGTATTTAGAAT 1500

Qy   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560
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Db   1501 GGGATCACGAGGAAAAGAGAAGGAAAGTGATTTTTTTCCACAAGATCTGTAATGTTATTT 1560

Qy   1561 CCACTTATAAAGGAAATAAAAA 1582
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Db   1561 CCACTTATAAAGGAAATAAAAA 1582


RESULT 7
AX018850
LOCUS       AX018850               1493 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent WO9943800.
ACCESSION   AX018850
VERSION     AX018850.1  GI:10042952
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1493)
  AUTHORS   Durrant,L.G. and Spendlove,I.
  TITLE     Tumor associated antigen 791tgp72
  JOURNAL   Patent: WO 9943800-A 5 02-SEP-1999;
            DURRANT LINDA GILLIAN (GB); SPENDLOVE IAN (GB); CANCER RES CAMPAIGN
            TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .1493
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             199. .1344
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                     /codon_start=1
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                     /db_xref="GI:10042953"
                     /translation="MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPN
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
BASE COUNT      401 a    355 c    355 g    382 t
ORIGIN

  Query Match             64.5%;  Score 1356;  DB 6;  Length 1493;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      5 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 64
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 TGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGC 197

Qy     65 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 124
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 CATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCG 257

Qy    125 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 184
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 GCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCC 317

Qy    185 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 244
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    318 AGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGT 377

Qy    245 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 304
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Db    378 AATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGAT 437

Qy    305 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 364
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Db    438 CTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGT 497

Qy    365 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 424
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Db    498 GCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCC 557

Qy    425 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 484
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Db    558 AGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATC 617

Qy    485 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618 ACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAA 677

Qy    545 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 604
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    678 GAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCAT 737

Qy    605 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 664
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Db    738 ATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGAC 797

Qy    665 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 724
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Db    798 TTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTG 857

Qy    725 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 784
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Db    858 CAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACG 917

Qy    785 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 844
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Db    918 TGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGAT 977

Qy    845 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 904
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Db    978 TGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACC 1037

Qy    905 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 964
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1038 ACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTAC 1097

Qy    965 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1024
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1098 CACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAAC 1157

Qy   1025 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1084
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Db   1158 CACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTT 1217

Qy   1085 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1144
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Db   1218 TCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATC 1277

Qy   1145 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1204
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Db   1278 TGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCT 1337

Qy   1205 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1264
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Db   1338 GACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTT 1397

Qy   1265 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1324
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Db   1398 TCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGC 1457

Qy   1325 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1360
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Db   1458 TTTCATTGTCTTTAAGATGTGTTAGGAATGTCAACA 1493
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RESULT 8
BC001288
LOCUS       BC001288                1357 bp    mRNA    linear   PRI 12-JUL-2001
DEFINITION  Homo sapiens, Similar to decay accelerating factor for complement
            (CD55, Cromer blood group system), clone MGC:5192 IMAGE:3460621,
            mRNA, complete cds.
ACCESSION   BC001288
VERSION     BC001288.1  GI:12654888
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1357)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-DEC-2000) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 4 Row: d Column: 2
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 181467.
FEATURES             Location/Qualifiers
     source          1. .1357
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                     /db_xref="taxon:9606"
                     /clone="MGC:5192 IMAGE:3460621"
                     /tissue_type="Cervix, carcinoma"
                     /clone_lib="NIH_MGC_12"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             80. .1225
                     /codon_start=1
                     /product="Similar to decay accelerating factor for
                     complement (CD55, Cromer blood group system)"
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                     /db_xref="GI:12654889"
                     /translation="MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPN
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
BASE COUNT      401 a    325 c    304 g    327 t
ORIGIN
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  Query Match           62.5%;  Score 1314;  DB 9;  Length 1357;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1314;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Db     15 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 74

Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     75 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 134

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    135 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 194

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    195 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 254

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    255 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 314

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    315 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 374

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    375 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 434

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    435 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 494
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Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    495 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 554

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    555 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 614

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    615 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 674

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    675 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 734

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
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Db    735 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 794

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    795 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 854

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    855 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 914

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    915 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 974

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    975 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1034

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1035 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1094

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1095 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1154

Qy   1141 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1155 TATCTGGGCACACGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCT 1214

Qy   1201 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1215 TGCTGACTTAGCCAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCT 1274

Qy   1261 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCA 1314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1275 AGTTTCTTAGACTTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCA 1328
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RESULT 9
I41330
LOCUS       I41330                2096 bp    DNA     linear   PAT 13-MAY-1997
DEFINITION  Sequence 1 from patent US 5624837.
ACCESSION   I41330
VERSION     I41330.1  GI:2081920
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2096)
  AUTHORS   Fodor,W.L., Rollins,S. and Squinto,S.P.
  TITLE     Nucleic acid encoding chimeric complement inhibitor proteins
  JOURNAL   Patent: US 5624837-A 1 29-APR-1997;
FEATURES             Location/Qualifiers
     source          1. .2096
                     /organism="unknown"
BASE COUNT      671 a    416 c    439 g    570 t
ORIGIN
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Query Match 59.1%; Score 1243; DB 6; Length 2096;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1393; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy     13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
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Db      1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy     73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy    133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy    193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy    253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy    313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
          |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy    373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy    433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy    493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy    553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
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Db    541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy    613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy    673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy    733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy    793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy    853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
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Db    841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy    913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960
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Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
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Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
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Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
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Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
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Db    1381 CATTCTTAGCACACCT 1396


RESULT 10
I49078
LOCUS       I49078                  2096 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5627264.
ACCESSION   I49078
VERSION     I49078.1  GI:2467541
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2096)
  AUTHORS   Fodor,W.L., Rollins,S. and Squinto,S.P.
  TITLE     Chimeric complement inhibitor proteins
  JOURNAL   Patent: US 5627264-A 1 06-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .2096
                     /organism="unknown"
BASE COUNT      671 a    416 c    439 g    570 t
ORIGIN

  Query Match           59.1%;  Score 1243;  DB 6;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
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Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
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Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
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Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
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Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

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Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
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Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
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Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
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Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
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Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
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Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
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Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
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Db    1381 CATTCTTAGCACACCT 1396


RESULT 11
I50941
LOCUS       I50941                  2096 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 10 from patent US 5643770.
ACCESSION   I50941
VERSION     I50941.1  GI:2472644
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2096)
  AUTHORS   Mason,J.M. and Squinto,S.P.
  TITLE     Retroviral vector particles expressing complement inhibitor
            activity
  JOURNAL   Patent: US 5643770-A 10 01-JUL-1997;
FEATURES             Location/Qualifiers
     source          1. .2096
                     /organism="unknown"
BASE COUNT      671 a    416 c    439 g    570 t
ORIGIN

  Query Match             59.1%;  Score 1243;  DB 6;  Length 2096;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1393;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 72
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Db       1 GCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGCGCGCCATGACCG 60

Qy      73 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 132
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Db      61 TCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGC 120

Qy     133 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTAC 180

Qy     193 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGT 240

Qy     253 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTA 312
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db     241 ACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTA 300

Qy     313 AGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 372
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGGCATGCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAA 360

Qy     373 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTA 420

Qy     433 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAAC 480

Qy     493 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCAT 540

Qy     553 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTG 600

Qy     613 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTT 660

Qy     673 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 TTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAA 720

Qy     733 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 TTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATT 780

Qy     793 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 ATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGC 840

Qy     853 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAAT 900

Qy     913 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAA 960

Qy     973 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACAC 1020

Qy    1033 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAA 1080

Qy    1093 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 CAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACA 1140

Qy    1153 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGTGTTTCACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGC 1200

Qy    1213 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 CAAAGAAGAGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGAC 1260

Qy    1273 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TTATCTGCATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTG 1320

Qy    1333 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 TCTTTAAGATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCA 1380

Qy    1393 CATTCTTAGCACACCT 1408
           ||||||||||||||||
Db    1381 CATTCTTAGCACACCT 1396


RESULT 12
HUMDAF
LOCUS       HUMDAF                  2017 bp    mRNA    linear   PRI 02-NOV-1994
DEFINITION  Human complement decay-accelerating factor (DAF) mRNA; 3' end.
ACCESSION   M15799
VERSION     M15799.1  GI:181462
KEYWORDS    complement decay-accelerating factor.
SOURCE      Human HeLa cell cDNA to mRNA, clones DF1 and DF2.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2017)
  AUTHORS   Medof,M.E., Lublin,D.M., Holers,V.M., Ayers,D.J., Getty,R.R.,
            Leykam,J.F., Atkinson,J.P. and Tykocinski,M.L.
  TITLE     Cloning and characterization of cDNAs encoding the complete
            sequence of decay-accelerating factor of human complement
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 84 (7), 2007-2011 (1987)
  MEDLINE   87175602
   PUBMED   2436222
COMMENT     Draft entry and computer-readable sequence [1] kindly provided by
            M.L.Tykocinski, 24-OCT-1988.
FEATURES             Location/Qualifiers
     source          1. .2017
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="1q32"
     gene            1. .2017
                     /gene="DAF"
     mRNA            <1. .2017
                     /gene="DAF"
                     /product="DAF mRNA"
     CDS             <1. .1131
                     /gene="DAF"
                     /note="decay-accelerating factor precursor"
                     /codon_start=1
                     /protein_id="AAA52167.1"
                     /db_xref="GI:181463"
                     /db_xref="GDB:G00-119-088"
                     /translation="PSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQPAL
                     EGRTSFPEDTVITYKCEESFVKIPGEKDSVTCLKGMQWSDIEEFCNRSCEVPTRLNSA
                     SLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKKKSCPN
                     PGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLPECREI
                     YCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEWSGPPP
                     ECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVSRTTKH
                     FHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
     sig_peptide     <1. .87
                     /gene="DAF"
                     /note="decay-accelerating factor signal peptide"
     mat_peptide     88. .1128
                     /gene="DAF"
                     /product="decay-accelerating factor"
BASE COUNT      654 a    390 c    414 g    559 t
ORIGIN      186 bp upstream of HindIII site.

  Query Match           55.9%;  Score 1175;  DB 9;  Length 2017;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1325;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      81 CCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTG 140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGCCCCGGCTGCTGCTGCTGGTG 60

Qy     141 CTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCC 200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTCCCCCAGATGTACCTAATGCC 120

Qy     201 CAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGT 260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATACTGTAATAACGTACAAATGT 180

Qy     261 GAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGATCTGCCTTAAGGGCAGT 320
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     181 GAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAGTGACCTGCCTTAAGGGCATG 240

Qy     321 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCGAGGTGCCAACAAGGCTAAAT 300

Qy     381 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATTTTCCAGTCGGTACTGTTGTG 360

Qy     441 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 GAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTCTATCACCAAAACTAACTTGC 420

Qy     501 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTAAAAAGAAATCATGCCCTAAT 480

Qy     561 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTGGCATATTATTTGGTGCAACC 540

Qy     621 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 ATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCTCGACTTCTAGTTTTTGTCTT 600

Qy     681 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 ATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAGAGTGCAGAGAAATTTATTGT 660

Qy     741 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGGAACGTGACCATTATGGATAT 720

Qy     801 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCATGATTGGAGAGCACTCTATT 780

Qy     861 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 TATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCCCACCACCTGAATGCAGAGGA 840

Qy     921 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 AAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAACCTACCACAGTAAATGTTCCA 900

Qy     981 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 1040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAAAAACCACCACACCAAATGCT 960

Qy    1041 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 CAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGCATTTTCATGAAACAACCCCA 1020

Qy    1101 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC 1160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 AATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTCTATCTGGGCACACGTGTTTC 1080

Qy    1161 ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAG 1220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ACGTTGACAGGTTTGCTTGGGACGCTAGTAACCATGGGCTTGCTGACTTAGCCAAAGAAG 1140

Qy    1221 AGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGC 1280
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AGTTAAGAAGAAAATACACACAAGTATACAGACTGTTCCTAGTTTCTTAGACTTATCTGC 1200

Qy    1281 ATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAG 1340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 ATATTGGATAAAATAAATGCAATTGTGCTCTTCATTTAGGATGCTTTCATTGTCTTTAAG 1260

Qy    1341 ATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTA 1400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 ATGTGTTAGGAATGTCAACAGAGCAAGGAGAAAAAAGGCAGTCCTGGAATCACATTCTTA 1320

Qy    1401 GCACACCT 1408
           ||||||||
Db    1321 GCACACCT 1328


RESULT 13
HUMDAFA
LOCUS       HUMDAFA                 2220 bp    mRNA    linear   PRI 02-NOV-1994
DEFINITION  Human decay-accelerating factor mRNA, complete cds.
ACCESSION   M30142
VERSION     M30142.1  GI:181464
KEYWORDS    Alu repeat; alternative splicing; decay-accelerating factor;
            membrane glycoprotein.
SOURCE      Homo sapiens cDNA to mRNA.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1  (bases 1 to 2220)
  AUTHORS Caras,I.W., Davitz,M.A., Rhee,L., Weddell,G., Martin,D.W. Jr. and
          Nussenzweig,V.
  TITLE   Cloning of decay-accelerating factor suggests novel use of splicing
          to generate two proteins
  JOURNAL Nature 325 (6104), 545-549 (1987)
  MEDLINE 87115845
   PUBMED 2433596
COMMENT   The gene for decay accelerating factor produces two proteins by
          alternative splicing.  The spliced out region is from position
          1147-1265.  The stop codon in this case is located at position
          1327-1329.  Though mRNAs do not have introns, the alternative
          coding region is indicated in the features table.
FEATURES             Location/Qualifiers
     source          1. .2220
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                     /db_xref="taxon:9606"
                     /map="1q32"
                     /cell_line="HeLa"
     mRNA            <1. .2220
                     /gene="DAF"
                     /note="G00-119-088"
     gene            join(66. .1146,1265. .1329)
                     /gene="DAF"
     CDS             join(66. .1146,1265. .1329)
                     /gene="DAF"
                     /codon_start=1
                     /product="decay-accelerating factor A"
                     /protein_id="AAA52168.1"
                     /db_xref="GI:181465"
                     /db_xref="GDB:G00-119-088"
                     /translation="MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPN
                     AQPALEGRTSFPEDTVITYKCEESFVKIPGEKDSVICLKGSQWSDIEEFCNRSCEVPT
                     RLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKWSTAVEFCKK
                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGHTCFTLTGLLGTLVTMGLLT"
     sig_peptide     66. .167
                     /gene="DAF"
                     /note="G00-119-088"
     mat_peptide     join(168. .1146,1265. .1326)
                     /gene="DAF"
                     /product="decay-accelerating factor A"
                     /note="G00-119-088"
     exon            <66. .1146
                     /gene="DAF"
                     /note="decay-accelerating factor precursor A"
                     /number=1
     mat_peptide     168. .1385
                     /gene="DAF"
                     /product="decay-accelerating factor A"
                     /note="G00-119-088"
     intron          1147. .1264
                     /gene="DAF"
                     /note="G00-119-088"
     repeat_region   1150. .1264
                     /note="Alu repeat (partial)"
     exon            1265. .>1329
                     /gene="DAF"
                     /note="G00-119-088"
                     /number=2
     polyA_signal    1410. .1415
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1693. .1698
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    1731. .1736
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_signal    2198. .2203
                     /gene="DAF"
                     /note="G00-119-088; putative"
     polyA_site      2220
                     /gene="DAF"
                     /note="G00-119-088"
BASE COUNT      681 a    455 c    475 g    609 t
ORIGIN

  Query Match             54.6%;  Score 1147;  DB 9;  Length 2220;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60

Qy      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
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Db     781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy     901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Db    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960

Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
Db   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080

Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
Db   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140

Qy   1141 TATCTGG 1147
Db   1141 TATCTGG 1147


RESULT 14
I09216
LOCUS       I09216                  2233 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 3 from Patent WO 8901041.
ACCESSION   I09216
VERSION     I09216.1  GI:588076
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2233)
  AUTHORS   Caras,I.W.
  TITLE     NUCLEIC ACID AND METHODS FOR THE SYNTHESIS OF NOVEL FUSION
            POLYPEPTIDES WITH A PHOSPHOLIPID ANCHOR DOMAIN
  JOURNAL   Patent: WO 8901041-A 3 09-FEB-1989;
FEATURES             Location/Qualifiers
     source          1. .2233
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BASE COUNT      695 a    455 c    475 g    608 t
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  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1147;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CCGCTGGGCGTAGCTGCGACTCGGCGGAGTCCCGGCGGCGCGTCCTTGTTCTAACCCGGC 60
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Qy     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120
Db     61 GCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTCGGGGAGCTGC 120

Qy    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180
Db    121 CCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGACTGTGGCCTTC 180

Qy    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240
Db    181 CCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTTCCCGAGGATA 240

Qy    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300
Db    241 CTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAGAAGGACTCAG 300

Qy    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360
Db    301 TGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAATCGTAGCTGCG 360

Qy    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420
Db    361 AGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACTCAGAATTATT 420

Qy    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480
Db    421 TTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGAGAACCTTCTC 480

Qy    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540
Db    481 TATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTCGAATTTTGTA 540

Qy    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600
Db    541 AAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGATGTACCAGGTG 600

Qy    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660
Db    601 GCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAATTATTTGGCT 660

Qy    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720
Db    661 CGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGACCCGTTGCCAG 720

Qy    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780
Db    721 AGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATAATTCAAGGGG 780

Qy    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840
Db    781 AACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAAGGATTCACCA 840

Qy    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900
Db    841 TGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAGTGGAGTGGCC 900

Qy    901 CACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACAGTTCAGAAAC 960
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Qy    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020
Db    961 CTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAAACCACCACAA 1020

Qy   1021 AAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGGACAACCAAGC 1080
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Qy   1081 ATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACTACCCGTCTTC 1140
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Qy   1141 TATCTGG 1147
Db   1141 TATCTGG 1147


RESULT 15
A65264
LOCUS       A65264                  2237 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 1 from Patent WO9735886.
ACCESSION   A65264
VERSION     A65264.1  GI:4531048
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 2237)
  AUTHORS   Watkins,N.J.
  TITLE     SURFACES WHICH PREVENT OR REDUCE COMPLEMENT ACTIVATION
  JOURNAL   Patent: WO 9735886-A 1 02-OCT-1997;
            IMUTRAN LTD (GB)
COMMENT     Other publication AU 1933897 19971017.
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                     KSCPNPGEIRNGQIDVPGGILFGATISFSCNTGYKLFGSTSSFCLISGSSVQWSDPLP
                     ECREIYCPAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIGEHSIYCTVNNDEGEW
                     SGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTKTTTPNAQATRSTPVS
                     RTTKHFHETTPNKGSGTTSGTTRLLSGSRPVTQAGMRWCDRSSLQSRTPGFKRSFHFS
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BASE COUNT      699 a    456 c    474 g    608 t
ORIGIN
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Query Match 52.2%; Score 1097; DB 6; Length 2237;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      51 CTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTC 110
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      50 CTAACCCGGCGCGCCATGACCGTCGCGCGGCCGAGCGTGCCCGCGGCGCTGCCCCTCCTC 109

Qy     111 GGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGAC 170
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     110 GGGGAGCTGCCCCGGCTGCTGCTGCTGGTGCTGTTGTGCCTGCCGGCCGTGTGGGGTGAC 169

Qy     171 TGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTT 230
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     170 TGTGGCCTTCCCCCAGATGTACCTAATGCCCAGCCAGCTTTGGAAGGCCGTACAAGTTTT 229

Qy     231 CCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG 290
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Db     230 CCCGAGGATACTGTAATAACGTACAAATGTGAAGAAAGCTTTGTGAAAATTCCTGGCGAG 289

Qy     291 AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAAT 350
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Db     290 AAGGACTCAGTGATCTGCCTTAAGGGCAGTCAATGGTCAGATATTGAAGAGTTCTGCAAT 349

Qy     351 CGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACT 410
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Db     350 CGTAGCTGCGAGGTGCCAACAAGGCTAAATTCTGCATCCCTCAAACAGCCTTATATCACT 409

Qy     411 CAGAATTATTTTCCAGTCGGTACTGTTGTGGAATATGAGTGCCGTCCAGGTTACAGAAGA 470
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     471 GAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTC 530
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     470 GAACCTTCTCTATCACCAAAACTAACTTGCCTTCAGAATTTAAAATGGTCCACAGCAGTC 529

Qy     531 GAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGAT 590
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Db     530 GAATTTTGTAAAAAGAAATCATGCCCTAATCCGGGAGAAATACGAAATGGTCAGATTGAT 589

Qy     591 GTACCAGGTGGCATATTATTTGGTGCAACCATCTCCTTCTCATGTAACACAGGGTACAAA 650
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Qy     651 TTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGAC 710
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Db     650 TTATTTGGCTCGACTTCTAGTTTTTGTCTTATTTCAGGCAGCTCTGTCCAGTGGAGTGAC 709

Qy     711 CCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATA 770
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     710 CCGTTGCCAGAGTGCAGAGAAATTTATTGTCCAGCACCACCACAAATTGACAATGGAATA 769

Qy     771 ATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAA 830
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     770 ATTCAAGGGGAACGTGACCATTATGGATATAGACAGTCTGTAACGTATGCATGTAATAAA 829

Qy     831 GGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAG 890
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     830 GGATTCACCATGATTGGAGAGCACTCTATTTATTGTACTGTGAATAATGATGAAGGAGAG 889

Qy     891 TGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACA 950
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     890 TGGAGTGGCCCACCACCTGAATGCAGAGGAAAATCTCTAACTTCCAAGGTCCCACCAACA 949

Qy     951 GTTCAGAAACCTACCACAGTAAATGTTCCAACTACAGAAGTCTCACCAACTTCTCAGAAA 1010
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Qy    1011 ACCACCACAAAAACCACCACACCAAATGCTCAAGCAACACGGAGTACACCTGTTTCCAGG 1070
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Qy    1071 ACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACT 1130
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Db    1070 ACAACCAAGCATTTTCATGAAACAACCCCAAATAAAGGAAGTGGAACCACTTCAGGTACT 1129

Qy    1131 ACCCGTCTTCTATCTGG 1147
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Db    1130 ACCCGTCTTCTATCTGG 1146
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